

QY	602	TATTAGCTAAAGGGGAAATATTATTAAGATGGAAGAGATCTGGTGTATTTGATTTGATTCAGTTAA	661
DB	734	TATTAAGTAAAGGGGAAAGCTATTAACAAATCGAAGATGATCGGTGATTTTCATTTTCAGTTAA	793
QY	552	TGTTAGTGTGCTTTCAGCTATATTTTAAACATCCACCTCCCATGCTGCTCAACAGAACCAT	721
DB	794	TGTTATGTGTCTTGATCTATTTTATTAACCTCTACGCTCCCATGCTGCTCAAGAGCAT	853
QY	722	ATAAAACAGCTGTATATCCATTAATATGGTTCCACCTCCCAACACCCAGCGAGGTTCAGAAACA	781
DB	854	ATAAAACAGCTGTATATCCATTAATATGGTTCCACCTCCCAACACCCAGCGAGGTTCAGAAACA	913
QY	782	AGAGTGTGAGGATATTAATAAATATAGAAATATGATCAAGAAATTTATGAAATTTCTCTGTATA	841
DB	914	GGAGTGTGAGGATATTAATAAATATAGAAATATGATCAAGAAATTTATGAAATTTCTCTGTATA	973
QY	842	AATCAATCTCAATCTAATATATCATCATGATCTCAAAAATCTTTATTTTCAAAAATTTTATATCTTT	901
DB	974	AATCAATCTCAATCTAATATATGATCTCAAAAATCTTTATTTTCAAAAATTTTATATCTTT	1033
QY	902	TTAGAAATCTCTTGAGCTTTGATACATCATATATGAGACTTCCAGAGGTTCGAAATCTTTTCTATA	961
DB	1034	TTAGAAATCTCTTGAGCTTTGATACATCATATATGAGACTTCCAGAGGTTCGAAATCTTTTCTATA	1093
QY	962	AATGATATCAAGAAATTTTATCTTTAAATATAAAGATATAGATGTAAATATTTTGTGATC	1021
DB	1094	AATGATATCAAGAAATTTTATCTTTAAATATAAAGATATAGATGTCAAGATATTTTGTGATC	1153
QY	1022	ATTATAAACTCTTTCAGACTGATCTATAGACAGTTTTCGAAACACAGACAGACACAGGAA	1081
DB	1154	ATTATAAACTCTTTCAGACTGATCTATAGACAGTTTTCGAAACACAGACAGACACAGGAA	1213
QY	1082	AAAGTAACCTTCATCAAGAGGTGAATGTAATTCCTCCACACACACCTCCAGCTTGGACTGTATA	1141
DB	1214	AAAGTAACCTTCATCAAGAGGTGAATGTAATTCCTCCACACACCTCCAGCTTGGACTGTATA	1273
QY	1142	TGAACATCTATCCAAATTTATTTATGATGATTTTAAATTCAGCAAGTGTATCAAGCTTCAGAAA	1201
DB	1274	TGAACATCTATCCAAATTTATTTATGATGATTTTAAATTCAGCAAGTGTATCAAGCTTCAGAAA	1333
QY	1202	ATCTGATCTCTCTATTTTAAACAATCTCCACAGTCAATCCAAAAGAAAGTATCTCAAAAGAG	1261
DB	1334	ATCTGATCTCTCTATTTTAAACAATCTCCACAGTCAATCCAAAAGAAAGTATCTCAAAAGAG	1393
QY	1262	TGAAGCATATAGCATACATCTTTAAAGCAAAATTTGCTTAAAGCTCTGGACAGAGGTGTG	1321
DB	1394	TGAAGCATATAGCATACATCTTTAAAGCAAAATTTGCTTAAAGCTCTGGACAGAGGTGTG	1453
QY	1322	TGAAATTTGATCTAAATATATCAAAATCTGATTTCAAAATTTTACCAAACTTCTCGAATG	1381
DB	1454	TGAAATTTGATCTAGCATACAGCATCAAAACTTGGAGTTTGGCTTGTATTCAGCAGTATCGAAT	1513
QY	1382	CGATCTTAAATTCAGAAAGAACCATATATCATTTCAAAATTTTACCAAACTTCTCGAATG	1441
DB	1514	CGATCTTAAATTCAGAAAGAACCATATATCATTTCAAAATTTTACCAAACTTCTCGAATG	1573
QY	1442	ATAAATTTTTCATATATCTTTATTCGGCTGGGCTTTGAGAGTTTGTAAATGGCCACATATA	1501
DB	1574	ACAACATTTTCATATATCTTTATTCGGCTGGGCTTTGAGAGTTTGTAAATGGCCACATATA	1633
QY	1502	GAAGAAATATTTAAAGGCTTTGATTTTACAAAGTCAAGCAAGTTTATCAAAAGCAG	1561
DB	1634	GAAGAAATATTTAAAGGCTTTGATTTTACAAAGTCAAGCAAGTTTATCAAAAGCAG	1693
QY	1562	ATGAGCTTAAATTTAAAGGCTTTGATTTTACAAAGTCAAGCAAGTTTATCAAAAGCAG	1621
DB	1694	ATGAGCTTAAATTTAAAGGCTTTGATTTTACAAAGTCAAGCAAGTTTATCAAAAGCAG	1753
QY	1622	AAAGCAACTTTCAGACACACAAACATATAAAATTTTATAGCAAGCTATGATCAATCATG	1681
DB	1754	AAAGCAACTTTCAGACACACAAACATATAAAATTTTATAGCAAGCTATGATCAATCATG	1813
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[illegible]

SEQUENCE CHARACTERISTICS:
 LENGTH: 2808 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYDROPHOBIC: NO
 ANTI SENSE: NO
 US 07 708 962 1

Query Match 1.98; Score 68.8; DB 1; Length 2808;

Best local Similarity 54.18; Pred. No. 1.2e-07;

Matches 170; Conservative 0; Mismatches 147; Indels 4; Gaps 1;

QY 1922 AGAAGGATGAAATAGCTGCTTTCATGTTTATATAAAGATGATGGTAGGCT 1981
 DB 1440 AAGAGGAAAGAAATGAGTCTTAGCAATATTTACAGAAAGGCTATCTTTGGCAA 1999
 QY 1982 APTGGGAGAAATATGCTTTCAGAGGCTGCTGCTGAGGAGGAGGAGGAGGAGG 2041
 DB 2030 GGTGAGGATTAAGGATGATGCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGG 2055
 QY 2042 TATGCTGAGGCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2101
 DB 2057 ACAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2116
 QY 2162 ATTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2161
 DB 2117 ATTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2176
 QY 2162 TAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2221
 DB 2177 GAGTTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2236
 QY 2222 TAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2241
 DB 2247 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2256

RESULT 14

US 08 106 494A 1

Sequence 1, Application US/08106494A

Patent No. 5457049

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRB2,

TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING

TITLE OF INVENTION: THEREFOR"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University of The Commonwealth

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/106 494A

FILING DATE: August 12, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mullins, J.G.

REGISTRATION NUMBER: 43,074

REFERENCE/DOCKET NUMBER: 6056-188

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568 8383

TELEFAX: (215) 568 5549

TELEX: No. 5457049

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3249 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

US-08-106-494A-1

Query Match 1.98; Score 68.2; DB 1; Length 3249;

Best local Similarity 54.08; Pred. No. 1.8e-07;

Matches 170; Conservative 0; Mismatches 148; Indels 4; Gaps 1;

QY 1922 AGAAGGATGAAATAGCTGCTTTCATGTTTATATAAAGATGATGGTAGGCT 1981
 DB 2112 ATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2171
 QY 1982 APTGGGAGAAATATGCTTTCAGAGGCTGCTGCTGAGGAGGAGGAGGAGGAGG 2041
 DB 2372 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2428
 QY 2042 TCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2101
 DB 2429 AAPTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2488
 QY 2402 ATTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2161
 DB 2489 ATTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2548
 QY 2362 TTAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2421
 DB 2549 AGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2608
 QY 2222 TCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2242
 DB 2609 ATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2629

RESULT 14

US-08-429-264-1

Sequence 1, Application US/08429264

Patent No. 5532440

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN

TITLE OF INVENTION: PRB2"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seigel, Gonda, Lavorata & Monaco, P.C.

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429,264

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,493

FILING DATE: August 12, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, D.A.

REGISTRATION NUMBER: 40,480

REFERENCE/DOCKET NUMBER: 6056-188

Genome version 5.1.4
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CGM nucleotide nucleotide search, using SW model

Run on: January 16, 2003, 15:20:22 : Search time 59.5955 seconds
(without alignments)
14,444,909 Million cell updates/sec

Filter: US 09 026 459A 40

Perfect score: 3392

Sequence: 1 GGAATGACGATTTTACTGCG.....AAATGACGATTTTACTGACT 3392

Scoring table: IDENTITY 90%

Gap: 10, 0, Gap-ext 1, 0

Search: 441,062 seqs, 15,338,481 residues

Total number of hits satisfying chosen parameters: 89,274

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: ISSUED PATENTS NA *

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- 2: /seq2_2/prodat/1/na/5B_5MB.seq *
- 3: /seq2_2/prodat/1/na/6A_5MB.seq *
- 4: /seq2_2/prodat/1/na/6B_5MB.seq *
- 5: /seq2_2/prodat/1/na/7A_5MB.seq *
- 6: /seq2_2/prodat/1/na/7B_5MB.seq *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Hit ID	Description
1	4222.4	95.0	3242	US 08 948 760-1	Sequence 1, Appl
2	4222.4	95.0	3242	US 08 948 760-2	Sequence 2, Appl
3	4222.4	95.0	3242	US 08 479 091-1	Sequence 1, Appl
4	4222.4	95.0	3242	US 08 479 091-2	Sequence 2, Appl
5	2691	79.3	2994	US 08 254 429-2	Sequence 2, Appl
6	2691	79.3	2994	US 08 482 627-4	Sequence 4, Appl
7	2691	79.3	2994	US 08 801 092-3	Sequence 3, Appl
8	2691	79.3	2994	US 09 415 113-4	Sequence 3, Appl
9	2689.4	79.3	2994	US 08 945 10357-1	Sequence 1, Appl
10	2688	79.2	2995	US 08 959 6387-7	Sequence 7, Appl
11	2688	79.2	2995	US 08 328 6338-7	Sequence 7, Appl
12	6818	2.0	2808	US 07 708 962-1	Sequence 7, Appl
13	681.2	2.0	3249	US 08 105 493A-1	Sequence 1, Appl
14	681.2	2.0	3249	US 08 329 264-1	Sequence 1, Appl
15	681.2	2.0	4853	US 08 832 883-1	Sequence 1, Appl
16	681.2	2.0	4853	US 08 832 877-1	Sequence 1, Appl
17	65.6	1.9	2808	US 08 152 721B-1	Sequence 1, Appl
18	59	1.7	721B	US 08 232 463-14	Sequence 14, Appl
19	51	1.5	3747	US 09 213 2949-2	Sequence 2, Appl
20	44.6	1.3	1803	US 09 144 001C 799	Sequence 799, Appl
21	44.6	1.3	15363	US 08 961 527 139	Sequence 139, Appl
22	44.4	1.3	20674	US 09 641 638-651	Sequence 651, Appl
23	44	1.3	19124	US 08 487 826B-13	Sequence 13, Appl
24	43.8	1.3	1056	US 09 134 001C 1550	Sequence 1550, Appl
25	43.2	1.3	690	US 08 030 607-202	Sequence 202, Appl
26	43.2	1.3	599	US 09 625 785-202	Sequence 202, Appl
27	43.2	1.3	599	US 09 439 313 202	Sequence 202, Appl

28	43.2	1.3	509	4	US 09 452 617A 202	Sequence 202, Appl
29	43.2	1.3	509	4	US 09 232 149A 202	Sequence 202, Appl
30	43	1.3	5852	1	US 07 867 106-2	Sequence 2, Appl
31	42.8	1.3	615	4	US 08 998 416 186	Sequence 186, Appl
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33	42.6	1.3	2689	4	US 09 234 827B 3	Sequence 3, Appl
34	42.4	1.2	1186	2	US 08 731 722 5	Sequence 5, Appl
35	42	1.2	665	2	US 08 883 795A 46	Sequence 36, Appl
36	42	1.2	1864	4	US 09 468 265 4	Sequence 4, Appl
37	41.8	1.2	1679	4	US 09 305 060 1	Sequence 1, Appl
38	41.4	1.2	19124	2	US 08 487 826B 13	Sequence 13, Appl
39	41.2	1.2	821	4	US 08 998 416 541	Sequence 541, Appl
40	41.2	1.2	837	4	US 08 998 416 288	Sequence 288, Appl
41	41.2	1.2	2030	2	US 08 705 937 7	Sequence 7, Appl
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43	40.6	1.2	4078	2	US 08 960 022 4	Sequence 4, Appl
44	40.6	1.2	6255	4	US 09 129 112 4	Sequence 4, Appl
45	40.6	1.2	12124	1	US 08 181 271A 56	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08 048-760-1
: Sequence 1, Application US/08048760
: Patent No. 5496741
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: APPLICANT: Hu, Shi-Xue
: TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and Methods for Tumor Suppressor Gene Therapy.
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 4
: APPROPRIATE ALLELES:
: ADDRESS: Penzance 3, Edwards
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036 2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/048,760
: FILING DATE: 1993/03/25
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Pousasant, Brian M
: REGISTRATION NUMBER: 28,452
: REFERENCE/BOOK NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790 9090
: TELEFAX: (212) 869 9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4242 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: Double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19...2469
US-08 048-760-1

Query Match 96.0%, Score 4222.4, Hit 1, Length 4242
Best Local Similarity 100.0%, Freq. No. 0;
Matches 4223, Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TELEFAX: 703-576-0300
2 INFORMATION FOR SEQ ID NO: 3:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 2994 base pairs
5 TYPE: nucleic acid
6 STRANDEDNESS: single
7 TOPOLOGY: linear
8 MOLECULE TYPE: cDNA
9 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
10 US 09 415-113-3

Query Match 79.4% Score 2691 DB 4 Length 2994

Best local similarity 100.0% Pos 0

Mismatches 2691 Conservative 0 Mismatches 0 Indels 0 Gaps 0

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22 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
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40 TTTTGTGATCATATAAATTTCTTCTATGATGATGATGATGATGATGATGATGATGATGATG
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15	024	TTTTAAATCTTTTATGAATTTCTCTCTGACACTTCTTAACATCTAAATGGACATTCAGACGCTTGAA	1083
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QY	1330	GTAAATGAAATGATTTCTTAAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	1389
26	194	GTAAATGAAATGATTTCTTAAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	1683
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30	234	TCAAAATCAAAAGTAAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	1923
QY	1630	CTTCAATCAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	1689
31	244	CTTCAATCAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	1983
QY	1690	AAATGATTAATTAAGGATTTAAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	1749
32	254	AAATGATTAATTAAGGATTTAAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	2043
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33	264	TTCTCAACCAATCAATTCAGACAGGATTTTAAACACTCCACATGATTTCTTAAACGA	2103

RESULT 10

RTSULT 10
US-08-959-638-7

US-08-939-038-7
; Sequence 7, Application US/08959638

; Patent No. 5932210

: GENERAL INFORMATION:

APPLICANT: Gregory, Richard J.

APPLICANT: WILLS, Ken N.

APPLICANT: Maneval, Daniel C.

TITLE OF INVENTION: Recombinant Adenoviral Vector and

TITLE OF INVENTION: Methods of Use

NUMBER OF SEQUENCES: 9

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QM protein: nucleic search, using frame_plus p2n model

Run on: January 18, 2003, 04:41:54 : Search time 62.1223 Seconds
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Perfect score: 4382

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 99868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787746

Minimum hit seq length: 0

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Post processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

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-LOGO=0 -LOCAL=0 -UNITS=bits -SUAP=1 -FNU=1 -WALRUX=0.5
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Database: Published Applications, NA:

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4382	100.0	4424	10	US-09-469-522-48 Sequence 48, Appl
2	4343	99.2	4451	10	US-09-469-522-46 Sequence 40, Appl
3	4343	98.9	4555	10	US-09-469-522-1 Sequence 1, Appl
4	4343	98.9	4539	9	US-09-954-531-143 Sequence 143, App

5	4323.5	98.7	2995	10	US-09-960-211-7 Sequence 7, Appl
6	4323.5	98.7	3564	10	US-09-469-522-50 Sequence 50, Appl
7	4217	96.2	3264	10	US-09-469-522-44 Sequence 54, Appl
8	4217	96.2	3243	10	US-09-469-522-42 Sequence 52, Appl
9	4217	96.2	3392	10	US-09-469-522-40 Sequence 40, Appl
10	4217	96.2	3455	10	US-09-469-522-28 Sequence 28, Appl
11	4192	95.7	3218	10	US-09-469-522-43 Sequence 43, Appl
12	4037	91.7	3114	10	US-09-469-522-36 Sequence 36, Appl
13	4007	91.4	3347	10	US-09-469-522-42 Sequence 42, Appl
14	3991	91.1	3377	10	US-09-469-522-46 Sequence 46, Appl
15	3984	90.9	3384	10	US-09-469-522-48 Sequence 48, Appl
16	3683	84.0	3161	10	US-09-469-522-44 Sequence 44, Appl
17	790	18.0	3460	9	US-09-292-766-37 Sequence 37, Appl
18	516.5	11.8	3747	10	US-09-770-657-1 Sequence 1, Appl
19	516.5	11.8	3747	12	US-10-025-676-2 Sequence 2, Appl
20	355.5	8.1	3209	10	US-09-220-091-4 Sequence 4, Appl
21	243	5.5	411	10	US-09-864-761-431 Sequence 431, Appl
22	218	5.0	129	10	US-09-864-761-14910 Sequence 19410, A
23	177.5	4.1	304	10	US-09-964-824-296 Sequence 296, App
24	153	3.5	5864	10	US-09-864-864-405 Sequence 405, App
25	148.5	3.4	3624	9	US-10-108-605-216 Sequence 216, App
26	148.5	3.4	10096	10	US-09-960-253-163 Sequence 163, App
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33	141	3.2	4754	10	US-09-982-091A-1 Sequence 1, Appl
34	138.5	3.2	2637	10	US-09-815-242-9859 Sequence 9859, App
35	138	3.1	8494	9	US-10-071-766-51 Sequence 51, Appl
36	134.5	3.1	2526	9	US-09-938-842A-1242 Sequence 1242, App
37	132	3.0	10300	10	US-09-960-253-145 Sequence 145, App
38	129.5	3.0	6504	10	US-09-801-468-55 Sequence 55, Appl
39	128	2.9	5362	10	US-09-801-468-59 Sequence 59, Appl
40	126.5	2.9	7497	10	US-09-960-253-175 Sequence 175, App
41	125.5	2.9	2988	10	US-09-815-212-4196 Sequence 4196, App
42	125.5	2.9	3030	10	US-09-815-242-8043 Sequence 8043, App
43	125.5	2.9	7792	12	US-10-034-690-459 Sequence 459, App
44	125	2.9	3774	10	US-09-925-432-47 Sequence 47, Appl
45	124.5	2.8	3247	9	US-10-071-766-39 Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-469-522-48
: Sequence 38, Application US-09-469-522
: Patent No. US20020151461A1
: GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED PEPTIDE-INDUCED MA TUMOR CELL LINES

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARI-11, White & Parkes

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4444

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA: US-09-469-522

APPLICATION NUMBER: US-09-469-522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>


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; APPLICANT: Watson, Zee
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; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 589290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/02/233,133
; PRIOR FILING DATE: 2000-09-18
; PCT: AF/02/233,133
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/00/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/00/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/00/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-954-531-143 (1-851) x US-09-954-531-143 (1-4839)

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138 1639 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1698
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SEQUENCE CHAP/TEPITIONS.
 LENGTH: 4266 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2502
 SEQUENCE DESCRIPTION: SPQ ID No. 34.
 US-09-469-522-34

Alignment Scores:

Prod. No.: 0 Length: 3264
 Score: 4217.00 Matches: 821
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.23% Indels: 0
 LB: 10 Gaps: 0

US-09-469-522-34 (1-951) x US-09-469-522-34 (1-3266)

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 400 AATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
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 171 GlySerProArqThrProArqArqGlyGlnAsnArqSerAlaArqIleAlaLysGlnLeu 190
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 460 GATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
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 191 AlaAspAspThrArqIleIleGluValLeuCysLysGluHisGlyCysAsnIleAspGln 210
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 520 GAAATGATACAAAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
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 580 GTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 639
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 231 SerAsnIleLeuProGluValGluAsnLeuSerLysAspTyrGluGluIleTyrLeuLys 250
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 640 TCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
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 700 AATAAGAT 759
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 271 IleAspSerPheGlnIleGluArqThrProArqLysSerAsnIleAspGluValIleAsn 290
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 760 ATAGAT 819

291 ValIleProProHisThrProValArqThrValMetAsnThrIleGlnIleGlnLeuMetMet 310
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 940 ACATGATATCAAAACAAACAACTATCTGAAACAGTGAAGGATATAGGATACATCTTAAAA 999
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 651 TyrLysAspLeuProHisAlaValGlnIleThrPhePheLysArqValLeuIleLysGluGln 670

[illegible]

GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunji

:
 : NUMBER OF SEQUENCES: 51
 :
 : CORRESPONDENCE ADDRESS:
 :

CITY: Houston
STATE: TX

ZIP: 77210-4433

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;
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent to Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Hidlet, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UICX:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3392 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 7..2628
 SPORINDIC DESCRIPTION: SEQ ID NO: 40.

US 09 469 522 40

Alignment Scores:

Pred. No.: 0 Length: 3392
 Score: 4217.00 Matches: 821
 Percent Similarity: 100.00% Conservat: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.24% Indels: 0
 DB: 10 Gaps: 0

US 09 026 459a 49 (1-851) x US-09-469-522-30 (1-3392)

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 71 MetSerArgLeuLeuLysLysValAspValLeuPheAlaLeuPheSerLysLeuGluArg 90
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 91 ThrCysGluLeuIleTyrLeuThrGluProSerSerSerIleSerThrGluIleAsnSer 110
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 191 GluAspAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 210

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 371 LeuLysValAlaLeuLeuTyrArgValMetGluSerMetLeuLysSerGlnLeuArg 490
 1186 CTGGAGCTCGCTTGATTTACCGAGTAATGGAACTCACTTAAATCAACACACACACACAC 1245
 391 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 410
 1246 TTATCCATTCAAAATTTTACCAAAATTTCTGAAATGACAAATTTTTCATATGCTTTATAG 1305
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 1366 TCTGGAAACAGATTTGCTTTCCCAATGCAATTCGCAATGCTTAAATTTTAAATTTTAT 1425
 451 PheTyrLysValIleGluSerPheIleLysAlaGlnGlyAsnLeuThrArgGlnMetIle 470
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 1546 CCTTTATTCATCTTATTAACAAATCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1605
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 1666 TCTCTGTGTAGATCTCTCAAAAGAAAAAGGCTTCAATCAAGCAAGCAAGCAAGCAAGCA 1725
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 1726 GCACACACACACACACACACCTTCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1785

Patent No. US20020151461A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong-Ji
 Hu, Shi-Xue
 Benedict, William F.
 Zhou, Yunli
 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1 0, Version #1 30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474 7577
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2454
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US 09-026-459A-39 (1-851) x US-09-469-522-3 (1-3218)

Alignment Scores:
 Prod. No.: 0 Length: 3218
 Score: 4192.00 Matches: 816
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.66% Indels: 0
 DB: 10 Gaps: 0

US 09-026-459A-39 (1-851) x US-09-469-522-3 (1-3218)

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CG	1300	AGTACATCTCAGAAATCTCATCTTCGACACAGATTGTCTTTCCCATGCAATCTTCAAATGTC	1359		
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CG	504	31yProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGluAsnAsnHis	523		
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CG	524	TheAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThrThr	543		
CG	1600	AAATGAAACATATATATGTTCTCTGTAGATCTCCAAAGAAAAGGTTCAATACG	1659		
CG	544	ArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGluThrGluLys	563		
CG	1660	CGTGTAATTTACTGCAAAATGACAGACACAAACCACTCAGCGTTCCAGACCCAGAA	1719		
CG	564	ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu	583		
CG	1720	CTCAATCAAACTCACCCTCTTACATGTTTTAAAAACGGTATCGCTAGCGTAATCTC	1779		
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CG	1840	TGACCGCTTTCGAAATACCTGACAAATGAGTATGAACTCATGAGACATCATGAGACACGCCATTC	1899		
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CG	1960	TTTAAATCATTTGTAACAGATATAGATATTTCTCATATTTCTTAGAGAGATTTTCAA	2019		
CG	664	ArgValLeuIleLysGluGluLeuTyrAspSerIleGluValPheTyrAsnSerValPhe	683		
CG	2020	CGTGTTTTGATCAAAACACAGAGATGATTTCTATTATGATATCTATTAACCTGGCTTC	2079		
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CG	2080	ATGATCATACTCAAAACAAATATTTGACGATAGCTTCCACCGAGCGGCTTACCTTGTCAT	2139		
CG	704	ProIleProHisIleThrArgIleSerProLysPheProSerProLeuArgIlePro	723		
CG	2140	CAATATATCTCATTTCTGAAATTTTAAAGTTTCTTCAATCTCAATCTACGGATTCCT	2199		
CG	724	GlyProAsnThrTyrLeuSerProMetLysSerProTyrLysHisSerGluGluLeu	743		
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CG	2260	ATATTAACAAAAATGACTCCAGATCAAGAACTCTAGTATCAATTCGTGAATCATTTCCG	2319		

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Db 2380 AGAAGVCTTCACAGGAACCAACCTCTCTAAACACACGAAAAAATACCTTTGATATTCAA 2439
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QY 824 LeuAlaGluMetThrSerIleArgIleArgMetGlnLysGlnLysMetAsnAspSerMet 843
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RESULT 14
US-09-469-522-46
? Sequence 46, Application US-09469522
? Patent No. US20020151461A1
? GENERAL INFORMATION:
? APPLICANT: Xu, Hong-Ji
? Hu, Shi-Xue
? Benedict, William F.
? Zhou, Yunli
? TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
? PROTEINS
? NUMBER OF SEQUENCES: 51
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Arnold, White & Durkee
? STREET: P.O. Box 4433
? CITY: Houston
? STATE: TX
? COUNTRY: USA
? ZIP: 77210-4433
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-99-469-522
? FILING DATE: 22-Dec-1999
? CLASSIFICATION: <unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/026,459
? FILING DATE: <unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Hibler, David W.
? REGISTRATION NUMBER: 41,071
? REFERENCE/DOCKET NUMBER: UIXC:506
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 512/418-3000
? TELEFAX: 512/474-7577
? INFORMATION FOR SEQ ID NO: 46:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3377 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 7..2613
? SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-469-522-46

Alignment Scores:
Prog. No.: 0 Length: 3477
Score: 790 Matches:

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Search completed: January 19, 2003, 05:40:19
Job time : 150.122 secs

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RESULT 2

US-09-469-522-1
Sequence 1, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Zhou, Yunli
Benedict, William F.
TITLE OF INVENTION: MODIFIED RETIN-BLASTOMA TUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210 4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469,522
FILING DATE: 22 Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: OTX:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-8000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2790

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GENERAL INFORMATION:
APPLICANT: XU, Hong-Ji
            Hu, Shi-Xue
            Benedict, William F.
            Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
                    PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Burkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
FLEXFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 base pairs
TYPE: nucleic acid
STRANDINESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..259
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Query Match
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Matches 3228; Conservative 0; Mismatches 0; Labels 0; Gaps
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Db 2135 TATTTTGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2135
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Db 2195 AAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2195
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QY 2574 AAGTAATATCTGGAGAGAGTGAATAATTCAGCAAACTGGCAGAAATGACTCTAC 2633
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QY 2634 TCGAATATGAAATGAAAGTGAATAATTCAGCAAACTGGCAGAAATGACTCTAC 2693
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RESULT 7

US-09-469-522-34

: Sequence: 34, Application: US/09469522

: Patent No.: US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Benedit, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01XC-506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-1000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3266 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2502
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-469-522-34

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Query Match:

Best Local Similarity 93.2%; Score 3225.4; DB 10, Length 3266;

Matches 3226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Sequence 4, Application US/09464522
 Patent No. US20020151461A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong Ji
 Ben, Shi Xue
 Benedict, William F.
 Zhou, Yunli
 TITLE OF INVENTION: MODIFIED PETINRIAST-MA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkin
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210 4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09464522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hubler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UIC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3218 base pairs
 TYPE: nucleotide acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..454
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US 09 464 522 3

Query Match
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4212; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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1990 CAACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 2049
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RESULT 11

US-09-469-522-42

Seq. 42, Affiliated, 03/03/463522

Patent No. US20020151461A1

GENERAL INFORMATION

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

REFERENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

2777 CACGCTTCTGTTTATGCGCACATTTAAATATCTTCAGTCTCTTTTGTGGATATAAAATGTG 2836
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Job time : 141.592 secs

GenCore version 5.1.3
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OM protein - nucleotide search, using frame-plus-p2n model

Run on: January 18, 2003, 04:41:54 : Search time 65.4803 Seconds
(without alignments)
6107.852 Million cell updates/sec

Title: US-09-026-459A-41

Porter score: 4631

Sequences: 1 MPKTPKIAATAAAAAAED.....TRMKKKNMSDETSNKKK 897

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Searched: 39868 seqs, 22944149 residues

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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4631	100.0	3461	10	US-09-469-522-40 Sequence 40, Appl
2	4605.5	99.4	3555	10	US-09-469-522-18 Sequence 1, Appl
3	4605.5	99.4	4839	9	US-09-954-531-143 Sequence 143, App
4	4595.5	99.2	2995	10	US-09-860-211-7 Sequence 7, Appl

5	4595.5	99.2	3554	10	US-09-469-522-50 Sequence 50, Appl
6	4417.5	95.4	3455	10	US-09-469-522-28 Sequence 28, Appl
7	4349	93.9	3323	10	US-09-469-522-38 Sequence 38, Appl
8	4307.5	93.0	3392	10	US-09-469-522-40 Sequence 40, Appl
9	4263	92.1	3377	10	US-09-469-522-46 Sequence 46, Appl
10	4256	91.9	3383	10	US-09-469-522-48 Sequence 48, Appl
11	4240	91.6	3347	10	US-09-469-522-42 Sequence 42, Appl
12	4219	91.1	3323	10	US-09-469-522-72 Sequence 32, Appl
13	4217	91.1	3266	10	US-09-469-522-34 Sequence 34, Appl
14	4192	90.5	4218	10	US-09-469-522-3 Sequence 3, Appl
15	4017	86.7	3113	10	US-09-469-522-46 Sequence 36, Appl
16	3912	84.5	3161	10	US-09-469-522-44 Sequence 44, Appl
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41	136	2.9	7497	10	US-09-960-253-175 Sequence 175, App
42	136	2.9	7792	12	US-10-044-090-359 Sequence 359, App
43	129.5	2.8	6594	10	US-09-801-368-55 Sequence 55, Appl
44	125.5	2.7	2988	10	US-09-815-242-4196 Sequence 4196, Ap
45	125.5	2.7	3030	10	US-09-815-242-8043 Sequence 8043, Ap

ALIGNMENTS

RESULT 1
US-09-469-522-40
Sequence 40, Application US-09469522
Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

NUMBER OF SEQUENCES: 51

COMPRESS/UNCOMPRESS:

ADDRESS/INVENTOR:

ADDRESS/INVENTOR: White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-DEC-1999

CLASSIFICATION: <Unknown>


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 730 MetGlnArgLeuLysThrAsnIleLeuGlnIleTyrAlaSerThrArgProThrLeuSer 749
 2287 ATGCAGAGACGATGAAACAAATATTTTCTGATGATGATGATGATGATGATGATGATGAT 2346
 750 ProIleProHisIleProArgSerProLysPheProSerProSerProSerProSerPro 769
 2347 CCAATACCTCAGATCTCTGAGGCTTACAGGCTTCTGATCTCTGATCTCTGATCTCTGAT 2406
 770 GlyLysAlaIleTyrIleSerProLeuLysSerThrThrLysLysSerIleLeuPro 789
 2407 GAGGGAACATCTATATTTCAACCTTCAAGAGTCCATATAAAATTTTCAAACTTCTGTA 2466
 790 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGlnSerPheGly 809
 2467 ACACCAACAAAAATGACTCCCAAGATCAAGAAATCTTAGATCAATTCGTGAATTCATGAG 2526

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730 MetGlnArgLeuLysThrAsnIleLeuGlnIleValSerProThrLeuSer 749
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RESULT 10

US-09-459-522-48
Sequence 48, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED REITHIN-PLASMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/066,459
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 99/066,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UDC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000


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QY 690 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGluThrGlnLys 609
DB 1496 GCGGAAATCTACAGCAAAAGTACACACACAAAGCAAGTCTGAGACACAGAA 1755
QY 610 ProLeuLysSerThrSerLeuSerLeuPheThrLysLysValTyrArgLeuAlaTyrLeu 629
DB 1756 GATTGAATGTACATCTCTTTCACCTGTTTATATATAAAGTGTATGGGTAGCCATCTC 1815
QY 611 ArgLeuAsnThrLeuGlySerGluArgLeuLeuSerGluHisProGluLeuGluHisLeu 649
DB 1816 GAGTAAATACACTTGTGAGAGGCTTCTGCTGAGACACCCAGAAATAGAAATATATATC 1875
QY 612 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 669
DB 1876 TGGACCCCTTCCACACACACCCCTGCAATGACTATGCACTCATGACACACAGCCATTG 1935
QY 613 AspinHisLeuMetLysSerMetTyrGlyTyrGlyLeuValLysAsnHisLeuLys 689
DB 1936 GATCAAAATATGATGCTTCTTATGATGATATATGTAATGTAATATATATATATATAA 1995
QY 614 PheLysLeuLeuValThrAlaTyrLysAsnLeuPheValAlaValGluThrPheLys 709
DB 1996 TTCAAAATCTTGAACAGATACAGAGATCTTCTCATGCTGCTGACAGAGACATTCAAA 2055
QY 615 ArgValLeuLeuLysGluGluGluTyrAspSerIleLeuValPheTyrAsnSerValPhe 729
DB 2055 GCGGCTTGTGATCAAGAGAGAGAGATGATGATATATATATATATATATATATATATAT 2115
QY 616 MetGlnArgLeuLysThrAsnLeuLeuGlnTyrAlaSerThrArgProThrLeuSer 749
DB 2116 ATGAGAGATCTGAAATCAAAATATATATGATGATGCTTCTCATGCTGCTGACAGAG 2175
QY 617 PheLeuHisLeuLeuArgSerProTyrLysPheProSerSerProLeuArgGluPro 769
DB 2176 GCAATATATGATCTGCAAGAGCTTTCANATTTTCTTAGTTCATCTTACGATCTCT 2235
QY 618 GlycylAsnHisLeuThrLeuSerProLeuLysSerProTyrLysSerGluLysLeuPro 789
DB 2235 GAGAGAGATCTGAAATCAAAATATATATGATGATGCTTCTCATGCTGCTGACAGAG 2295
QY 619 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysSerPheGly 809
DB 2296 ACAACAAACAAATGATCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2355
QY 620 ThrSerGluLysPheGlnLysIleLeuGlnMetValCysAsnSerAspArgValLys 829
DB 2355 ACCTCTGAGAGATCTGCAAGAGATCTGCAAGAGATCTGCAAGAGATCTGCAAGAGAT 2415
QY 621 ArgSerAlaValGlySerArgProLeuLysProLeuLysLysLeuArgPheAspIleGlu 849
DB 2416 AGAAGTCTGCAAGAGATCTGCAAGAGATCTGCAAGAGATCTGCAAGAGATCTGCAAG 2475
QY 622 GlySerAspGlnAlaAspGlySerLysHisLeuProGlyLysSerLysPheGlnLys 869
DB 2476 GATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2535
QY 623 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 889
DB 2535 CTGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2595
QY 624 AspThrSerAsnLysGluGluLys 897
DB 2596 CATACGTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2619

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RESULT 11

US-09-469-522-42

Sequence 42, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPL. ATION NUMBER: 05, 17, 429, 522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

ACHILGALICA NUMBER: 03/046,459

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 3347 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2583

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-469-522-42

Alignment Scores:

Fold. No.:

Score: 0

Percent Similarity: 4240.00

Best Local Similarity: 93.65%

Query Match: 92.43%

Indels: 91.56%

Gaps: 10

Length: 3347

Matches: 829

Conservative: 11

Mismatches: 19

Indels: 38

Gaps: 3

US-09-026-459a-41 (1-897) x US-09-469-522-42 (1-3347)

QY 1 MetProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaGluPro 20

DB 7 ATGCGCCCAACAAACCCCGGCAAAATGAGGAGGAGAGAGAGAGAGAGAGAGAGAG 66

QY 21 ProAlaProProProProProProProProProGluGluAspProGluGlnAspSerGlyProGln 40

DB 67 CCGGACCG 126

QY 41 AspLeuProLeuValArgLeuGluPheGluGluGluGluGluGluGluGluGluGlu 60

DB 127 CACTTCCT 186

QY 61 CysGlnLysLeuLysIleProAspHisValArgGluArgAlaIleProLeuValAspLeuAsp 80

DB 187 TGTCAAAATTAATAATATAATATATATATATATATATATATATATATATATATATAT 234

QY 81 GluMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhe 100

DB 235 -----ACITGGGAGAAAGT----- 249

QY 101 PheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLeu 120

1273 GAGTTTAAATGGGCAATATAGAGAGATACATCTCGAATCTTGATTCGGAAAGAT 1442
 481 LeuSerPheProTyrPheLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 500
 1333 TTGCTTTTCCCAICGATTCGAAATCGCTTAATTTAAAGACCTTTGATTTTAAAGG 1492
 501 TleGluSerPheIleLysAlaIleGluLysLeuLeuThrAspIleMetIleLysHisLeuGlu 520
 1393 ATCCAAATCTTTTATCTAAAGCAAGACCAACCTCCACACAGCAAAAGCAATATACAA 1452
 521 ArgCysGluHisAspIleMetGluSerLeuAlaIlePheSerAspSerProLeuPheAsp 540
 1453 CGATGTGAACATCGAATCATGGAAATCGCTTGCATGGCTCTCCAGATTACGTTATTGAT 1512
 541 LeuIleLysGlnSerLysAspIleGluLysProIleThrAspHisIleGluLysAlaLysPro 560
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 561 LeuAsnLeuProLeuGluAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArg 580
 1573 CTAAATCTCTCTCCCAATTAATCACTGACAGACATATGTAATCTCTCTCTGTAAGA 1642
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 641 GluHisProGluLeuGluHisIleIleIleThrPheLeuPheGlnHisPheLeuLeuAsnGlu 660
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 661 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIle 680
 1873 TATCAACTCACTACAGACAGAGCATTTCCACCAAAATTAAGAAGCTCTCTCTCTCTCT 1942
 681 CysLysValLysAsnIleAspLysLysPheLysIleIleValThrAlaIleLysAspLeu 700
 1943 TCCAAAGTCAACAAATATAGACCTTAAATTAATAATCATCTGTAACAGCAATATACAA 1992
 701 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluLeuLeuTyrAspSer 720
 1993 CTTATGCTGTTCCAGACACATTCAAAGTGTTTTTGATCAAAAGAGAGAGATGATTCT 2052
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 2243 CCATATAAATTTCCAAACCTCTCCCAATATCAACAAACAAACAAATATATATATATAT 2292
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 2293 TTAGTATCAATTTGGTGAATCATCTGGGACTTCTGAGAGATTCACAGAAATATATATAT 2352
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 161 LysValSerTyrPheThrPheLeuLeuAlaLysGlyGluValLeuGluMetGluAspAsp 180
 473 AAATTTTCTGGATCACTATTTTATTAAGCTAAAGGGAGATATATACAAATGGAGATGAT 432
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 221 ThrProArgValGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThr 240
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 241 ArgIleIleGluValLeuPheCysLysGlnHisCysAsnIleAspGlnValLysAsnVal 260
 613 AGAATATTGAAGTCTCTCTGTAAGAACATGAATGTAATATATAGATGAGTGGAATAATGTT 672
 261 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeu 280
 673 TATTTCAAAAATTTATAGCTTTTATGAAATCTCTGTCGCTGCACTTCACTTAATGCACTT 732
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 733 CCAAGGTTGAAGATCTTTCTTAACAGATAGAGAAATTTATCTTAATAATAAGATCTA 792
 301 AspAlaArgIleGluPheGluAspHisAspLysThrLeuGlnThrAspSerIleAspSerPhe 320
 793 GATGCAACATATTATTTGATCATGATAAACCTCTCTGAGACTGATCTATAGACAGTTT 852
 321 GluThrGlnArgThrProArgLysSerAsnLeuAspGlnValValAsnValIleProPro 340
 853 CAACAACACACAAACACCAACAAAGTAAAGCTGATCAAGAGGTGAATCTAATTCCTCCA 912
 341 HisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 360
 913 CACATCTGAGTTAGACTGTTATCAACACTATCTCAACCAATTAAGATGATTTTAATTTCA 972
 361 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnPro 380
 973 GCAATGATCAACCTTCAAAATCTGATTTCTATTTAAACAACTCAACAGTGAATCCA 1032
 381 LysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 400
 1033 AAACAAAGCTATCTGAAACACGACGACGATACGATACATCTTTAAAGACAAATTTGCT 1092
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 1093 AAGGCTGTGGACACAGGTTGGTGGAAATTTGATCAACAGGATACAAACTTGGAGTCTGC 1152
 421 LeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGln 440
 1153 TTGATTAACGAGTAATGCAATGCTATGTTAAATCAAGAAAGAAAGATATATCATTCAT 1212
 441 AsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 460
 1213 AAATTTTCAACCTCTGCAATGCAACAAATTTTCAATATGCTTTATTTGGGCTGGCTCTT 1272
 461 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAsp 480

QY 442 ThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAla 361
 DB CC
 DB 787 ACICGACGATAGACACGATATGACACACATCCACAAATTAATGATGATTTTAAATTCACCA 846
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 DB CC
 DB 847 AGTGATCAAGCTTCAGAAAATCGATTTGCTATTTTAAACACTGACACAGGAATCCAAA 906
 QY 482 GluSerIleLeuLysAsnValLysAspIleGlyTyrIlePheLysGlnLysPheAlaLys 401
 DB CC
 DB 487 GAAAGATATATGAAGAAAGTCAAGAGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 966
 QY 492 AlaValIleGlyLeuLysValGlnIleGlySerGlnAsnArgTyrLysLeuGlyValArgLeu 421
 DB CC
 DB 497 GCGTGGGACAGAGATGAGTGGGAGAAATGGATACACAGCAATCAACCTGGAGTGGCTG 1026
 QY 422 TyrTyrArgValMetGluSerMetLeuLysSerGlnGluGluArgLeuSerIleGlnAsn 441
 DB CC
 DB 1027 TATTACGAGTAATGAAATGATGCTTAAATCAGAAAGAACGATTATCCATCCAAAT 1086
 QY 442 PheSerIleLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGlu 461
 DB CC
 DB 1087 TTTAGAAACTTCTGGAAGACACATTTTTCATATGCTTTTATGGGAGTGGCTCTTGAG 1146
 QY 462 ValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 481
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 DB 1147 GTTCTAAAGGACATATATACACAGATACATCTTCATCAATCTTCATCTGGAAACAGATTG 1206
 QY 482 SerPheProIleLeuLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIle 501
 DB CC
 DB 1207 TCTTGGCATGGATTCTGAAAGTGGCTTAAATTTAAAGAGCTTTGATTTTACAAAGTGATC 1266
 QY 502 GluSerPheIleLysAlaLeuGlyAsnLeuThrArgGluMetIleLysHisGluArg 521
 DB CC
 DB 1267 GAAATTTTATTAAGAAAGAGAGANATTGCAANASAAATGATAAANATTTTANAGCA 1326
 QY 522 CysGlnHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeu 541
 DB CC
 DB 1327 TGGAAATGCGAAATACGAAATGAGCTTATGAGCTGCTGACATGACCTTTATTTGATCTT 1386
 QY 542 IleLysGlnSerLysAspArgGlnGlyProThrAspHisLeuIleSerAlaCysProLeu 561
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 DB 1387 ATTAAAATACAAAG 1446
 QY 562 AsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 581
 DB CC
 DB 1447 AATCTTCTCTCCAGAAATAATCAATGCAAGAAATATATCTTCTTCTTCTTCTTCTTCTTCT 1506
 QY 582 ProLysGlyLysGlySerThrTrpArgValAsnSerThrAlaAsnAlaGluThrGlnAla 601
 DB CC
 DB 1507 GCAAGAAAAAGGCTTCACTACCGGTGTAATTTCTACTCCAAATGACAGAGACACAAAGCA 1566
 QY 602 ThrSerAlaPheThrIleLysProLeuTyrSerThrSerLysSerLeuPheTyrLys 621
 DB CC
 DB 1567 ACCTCAATCTCCAG 1626
 QY 622 LysValTyrArgGlnAlaLysArgAlaLeuAsnHisThrLysGlnArgLeuSerGlu 641
 DB CC
 DB 1627 AAAATGATGAGTATGATATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1686
 QY 642 HisPheGlnLeuGlnIleGlnThrThrLeuPhePheHisThrLeuGlnArgLeuTyr 661
 DB CC
 DB 1687 GAGGAGAAATTAAGAAATATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1746
 QY 662 GlnLeuMetArgAlaPheGlnLeuAspGlnIleMetLeuMetCysSerMetTyrGlyLys 681
 DB CC
 DB 1747 GAAATCATATGAG 1806
 QY 682 LysValLysAsnIleAspLeuLysPheLysIleLeuValThrAlaTyrLysAspLeuPro 701
 DB CC
 DB 1807 AAAGTGAAGATATATGAGCTTAAATTCAAATCATTTGTAACAGACATACAAAGGATCTTCT 1866

QY 702 HisAlaValGlnGlnThrPheLysArgValLeuIleLysIleGlnGlnThrAspSerIle 721
 DB CC
 DB 1867 CATGCTGCTTACAGACACATTCACAAAGCTTTTGAATCAAGACAGACAGATATCTAT 1926
 QY 722 IleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAla 741
 DB CC
 DB 1927 ATAGTATTTCTATAACTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1986
 QY 742 SerThrArgProThrLeuSerProIleProHisIleProArgSerProLysThrIle 761
 DB CC
 DB 1987 TCCACAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2046
 QY 762 ProSerSerProLeuArgIlePheGlyGlyAsnIleTyrIleSerGlnGlySerThrPro 781
 DB CC
 DB 2047 CCTACTTCACCTTACGATCTCTGAGGAGACATCTATTTTCACTCCCTCGAAGAGTCCA 2106
 QY 792 TyrLysIleSerGlnGlyLeuThrPheThrPheLysMetThrProArgSerArgIleLeu 801
 DB CC
 DB 2107 TATAAAATTTTCAAGCTCTGCAAAAGCAAAATCAAAATCAAAATCAAAATCAAAATCAAA 2166
 QY 802 ValSerIleGlyGluSerPheGlyThrSerGlnGlySerPheLysIleAsnGlnMetVal 821
 DB CC
 DB 2167 GATCAATTTCTGCAATCAATCTGAGACATCTGAGACATCTGAGACATCTGAGACATCTGAG 2226
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 DB CC
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 QY 842 LysLysIleAsnArgPheAspIleGlyGlySerAspGlnAlaAspGlySerLysHisGlnPro 861
 DB CC
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 QY 862 GlyGlnSerLysPheGlnGlnLysGlnAlaGluMetThrSerThrArgThrArgMetGln 881
 DB CC
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 DB CC
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RESULT 15

US-09-459-544-36

: Sequence 36, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yuuli

: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Durkee

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

: COUNTRY: USA

: ZIP: 77210-4433

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent in Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: 09/046,952

: FILING DATE: 22-Dec-1999

: CLASSIFICATION: <Unknown>

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 09/026,459

: FILING DATE: <Unknown>

: ATTORNEY/AGENT INFORMATION:

: NAME: Bibler, David W.

PERESTIMATION NUMBER: 41,071
REFERENCE/POCKET NUMBER: 01X0:506

TELEPHONE NUMBER: 512/474-3000

TELEPHONE: 512/474-7577

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CY 717 GluTyrAspSerIleIleValPheTyrAsuSerValPheMetuGluArgLeuLysThrAsn 736
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UU 1807 GAGTATGATCTATTATAGTATCTATAAAGCTCGCTCTCATGAGAGACAGTGAACAAAT 1866

CY 717 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 756
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UU 1867 ATTTGGAGTAGCTTCACACAGATCTCTATCTATCTATCTATCTATCTATCTATCTATCT 1926

CY 717 SerProTyrLysPheProSerSerProLeuArgIleProGlyClyAsnIleClyIleSer 776
UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
UU 1927 AGCCCTTACAAAGTTTATATATATATATATATATATATATATATATATATATATAT 1986

CY 717 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 796
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UU 1987 CCCCIGAGAGATCCCAATATAAAATTCAGAGAGCTCTCCCAACACCAACAAAAATGACTCCA 2046

CY 717 ArgSerArgIleLeuValSerIleGlyGluSerPheClyThrSerGluLysPheGlnLys 816
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UU 2047 AGATCAAGAAATCTTAGTATCAATATGATGAATATTCGGAATCTTCGAAGTTCTGAGAAA 2106

CY 817 IleAsnGlnMetValCysAsnSerAspArgValIleuLysArgSerAlaGluGlySerAsn 836
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UU 2107 ATAAATCAGATGATATATATATATATATATATATATATATATATATATATATATAT 2166

CY 817 ProProLysProLeuGlyLysLeuAlaArgPheAspIleGluGlySerAspGluAlaArgGly 856
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UU 2167 CCGCCIAAAGCAGTGAAGAAAACCTACGCTTTGATATTCAGGATCAGATCAAGTCAATCCA 2226

CY 817 SerLysHisLeuProGlyGlySerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 876
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UU 2227 AGTAAATATCTGGAGAGAGAGTCTTAAATTTAGTAAATTTAGTAAATTTAGTAAATTT 2286

CY 817 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 896
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CY 897 Lys 897
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UU 2347 AAA 2349

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Job time : 157.46 secs

GenCore version 5.1.4
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om nucleic nucleic search, using sw model

Run on: January 16, 2003, 15:29:22 : Search time 91.4372 seconds
(without alignments)
16420.741 Million cell updates/sec

Init file: US-09-026-459A-42

Perfect score: 3447
Sequence: 1 CGGCGATGCGGCGGAAAAA.....AAATGAGGATTATGATACT 3347

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 49808 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum db seq length: 0

Maximum db seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /com2/6/prodat/1/pubpna/pcl_NEW_UB.seq.*
3: /com2/6/prodat/1/pubpna/us06_NEW_PUB.seq.*
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12: /com2/6/prodat/1/pubpna/us10_pucomB.seq.*
13: /com2/6/prodat/1/pubpna/us60_NEW_PUB.seq.*
14: /com2/6/prodat/1/pubpna/us60_pucomB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3447	100.0	3447	10	US-09-469-522-42 Sequence 42, Appl
2	3126.8	94.4	3554	10	US-09-469-522-50 Sequence 50, Appl
3	3126.8	94.4	4555	10	US-09-469-522-1 Sequence 1, Appl
4	3126.8	94.4	4839	9	US-09-454-531-143 Sequence 143, Appl
5	4111	92.9	3377	10	US-09-469-522-46 Sequence 46, Appl
6	4109	92.9	3461	10	US-09-469-522-40 Sequence 40, Appl
7	4066.2	91.6	3323	10	US-09-469-522-48 Sequence 38, Appl
8	4019.8	90.2	3455	10	US-09-469-522-28 Sequence 28, Appl
9	4006	89.8	4113	10	US-09-469-522-46 Sequence 36, Appl
10	4006	89.8	4216	10	US-09-469-522-3 Sequence 3, Appl
11	4006	89.8	4266	10	US-09-469-522-44 Sequence 34, Appl
12	4006	89.8	4329	10	US-09-469-522-32 Sequence 32, Appl
13	4006	89.8	4392	10	US-09-469-522-40 Sequence 30, Appl
14	2965	86.6	3161	10	US-09-469-522-44 Sequence 44, Appl
15	2911.4	87.0	3383	10	US-09-469-522-48 Sequence 48, Appl
16	2429.2	72.6	2995	10	US-09-860-211-7 Sequence 7, Appl
17	428	12.8	451	9	US-09-746-692-7740 Sequence 7740, Ap
18	142.2	4.2	411	10	US-09-864-761-3141 Sequence 3141, Ap
19	129	3.9	129	10	US-09-864-761-1910 Sequence 1910, A

Sequence 296, App
Sequence 47, Appl
Sequence 2546, Ap
Sequence 1, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 342, App
Sequence 34, App
Sequence 4, Appl
Sequence 11218, A
Sequence 14521, A
Sequence 4592, Ap
Sequence 154, App
Sequence 3014, Ap
Sequence 5558, Ap
Sequence 11244, A
Sequence 5785, Ap
Sequence 1, Appl
Sequence 12458, A
Sequence 5218, Ap
Sequence 2769, Ap
Sequence 4147, Ap
Sequence 4050, Ap
Sequence 749, App

ALIGNMENTS

RESULT 1

US-09-469-522-42

: Sequence 42, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: In, Shi Xue

: Benedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MUTATED EELIN BLAST-MA JUM K SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Burke

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

: COUNTRY: USA

: ZIP: 77210-4433

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent Release #1.0, Version #1.40

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US-09-469-522

: FILING DATE: 22-Dec-1999

: CLASSIFICATION: Unknown

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 09/026,459

: FILING DATE: Unknown

: ATTORNEY/AGENT INFORMATION:

: NAME: Hibel, David W.

: REGISTRATION NUMBER: 41,071

: REFERENCE/DOCKET NUMBER: UI-XC-506

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 512/418-4000

: TELEFAX: 512/474-7577

: INFORMATION FOR SEQ ID NO. 42:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3447 base pairs

: TYPE: nucleic acid

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QY	402	AAAGAGGAGCTAATCAAAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	461						
Db	478	AAAGAGGAGAGATTAATCAAAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	437						
QY	492	GGGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	521						
Db	498	GGGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	497						
QY	522	AGCTTTAT	581						
Db	498	AGCTTTAT	557						
QY	582	AGGATATAGAAAAAAT	641						
Db	598	AGGATATAGAAAAAAT	617						
QY	642	TGAATGTAAT	701						
Db	618	TGAATGTAAT	677						
QY	702	TTCCTTGTGAT	761						
Db	678	TTCCTTGTGAT	737						
QY	762	GAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	821						
Db	748	GAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	797						
QY	822	AACTGTTGAGAT	881						
Db	798	AACTGTTGAGAT	857						
QY	882	CTTGATATAG	941						
Db	858	CTTGATATAG	917						
QY	942	TAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1001						
Db	918	TAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	977						
QY	1002	TTCCTTGTGAT	1061						
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Db	1218	TTTCAT	1277						
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QY	1602	TGCACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1661						
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Db	1638	TCTAAATTTACTGCAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG	1697						
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QY	1782	GCTAAATTTACTGCTCTTTTCACTGCTTTTCACTGCTTTTCACTGCTTTTCACTGCTTTTCACTGCTTTT	1841						
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QY	1962	CAAAATTAATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2021						
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QY	2082	GCACAGATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2141						
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QY	2142	AATACCTCAGATTCCTGCAAGCTCTTACAACTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2201						
Db	2118	AATACCTCAGATTCCTGCAAGCTCTTACAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2177						
QY	2202	AGGCAATATCTATATTCACAGCTTCAACAGCTTCAACAGCTTCAACAGCTTCAACAGCTTCAACAGCTTCA	2261						
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RESIDUE 1-34
US-09-469-522-30
Sequence 30, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yueli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UIXC:506
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..3638
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-469-522-30

Query Match 89.8% Score 3006; Db 10; Length 3492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 367 ATCTACTGAAATAAATCTGCAATGGTCGTAAGAACTTCTTGGCAGCACAATTTTATGAC 446
QY 402 TAAAGGGGAAGTATTAAATAGGGAATGATGATGATGATGATGATGATGATGATGATGATG 461
DB 447 TAAAGGGGAAGTATTAAATAGGGAATGATGATGATGATGATGATGATGATGATGATG 506
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Genforce version 5.1.3
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nm protein nucleic search, using frame_plus.p2n model
Run on: January 18, 2003, 04:31:54 : Search time 57.7433 Seconds
(without alignments)
6107.852 Million cell updates/sec

File: us-09-026-459a-51

Perfect score: 4798
Sequence: 1 MFPEKPKKIAIAAAAAAEP.....TRMOKRMNDSMTSNKEEK 928

Scoring table:
BLOSUM62
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Ygapop 10.0 : Ygapext 0.5
Fgapop 6.0 : Fgapext 7.0
Delop 6.0 : Delext 7.0
Searched: 93868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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DB=publisedApplications NA -GPMI-fastap -SUFFIX-rnpb -MINMATCH=0.1
-LOCAL=0 -XGAPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62
-TRANS=human40 cdi -LISP=45 -LOCAL=0 -GPMI=200 -THE_SCORE=pet -THE_MAX=100
-THE_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcg -NORM=ext -HEAPSIZE=500 -MINLEN=0
MAXLEN=2000000000 -DSFP=US09026459 seqn 1 1 500 -rnat 16012003 152139 23369
NCPD=6 -ICPD=3 -NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIDOG
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FCGAPEXT=7 YGAPOP=10 YGAPEXT=0.5 -DELDEL=6 -DELEXT=7

Database :

PublishedApplications_NA:

Seq	Score	Match	Length	DB	Description
1	4798	100.0	4554	10	US-09-469-522-50
2	4787	99.8	4555	10	US-09-469-522-1
3	4787	99.8	4839	9	US-09-954-531-143
4	4777	99.6	2995	10	US-09-860-211-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	Description
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2	4787	99.8	4555	10	US-09-469-522-1
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4	4777	99.6	2995	10	US-09-860-211-7

Seq	Score	Match	Length	DB	Description
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6	4595.5	95.8	3461	10	US-09-469-522-40
7	4489	93.6	3392	10	US-09-469-522-40
8	4444.5	92.6	3477	10	US-09-469-522-46
9	4437.5	92.5	3384	10	US-09-469-522-48
10	4398.5	91.7	3347	10	US-09-469-522-42
11	4357	90.8	3323	10	US-09-469-522-42
12	4323.5	90.1	3323	10	US-09-469-522-48
13	4263	88.8	3266	10	US-09-469-522-44
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15	4088.5	84.8	3161	10	US-09-469-522-44
16	4017	83.7	3113	10	US-09-469-522-46
17	810.5	16.9	3960	9	US-09-292-758-47
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19	516.5	10.8	3747	12	US-10-025-676-2
20	384.5	8.0	3259	10	US-09-420-091-4
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23	177.5	3.7	304	10	US-09-964-824A-296
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25	152	3.2	10096	10	US-09-960-254-163
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28	147	3.1	10211	10	US-09-954-456-1153
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35	141	2.9	4754	10	US-09-982-091A-1
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37	138.5	2.9	2647	10	US-09-815-242-9859
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39	134	2.8	6384	10	US-09-801-368-57
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ALIGNMENTS

RESULT 1
US-09-469-522-50
: Sequence 50, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED ETHYLENEDIAMINE DIMER DEPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Azevedo, White & Barker
: STREET: P.O. Box 4443
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4443
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09469, 522
: FILING DATE: 22-Dec 1999
: CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA: 09/026,459
 FILING DATE: <UNKNOWN>
 ATTORNEY/AGENT INFORMATION:
 NAME: HIBLER, DAVID W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-0000
 TELEFAX: 512/474 7577
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3554 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2790
 SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 S 09 469 522 50

[illegible]

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DB 247 GTTTCATCTGGATGATGAAATATGAGAGATATATATCAAAAGAAAAAGAAATATGGAGA 406
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DB 307 ATCTGTAATTCACAGAGTACCTAGATGATGATGATGATGATGATGATGATGATGATGAT 366
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2898 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2931

RESULT 4
US-09-860-211-7
Sequence 7, Application US/09860211
Patent No. US-0930137212A1
GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
Wills, Ken N.
Maneval, Daniel C.
TITLE OF INVENTION: Recombinant Adenoviral Vector and Methods of Use
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,211
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,673
FILING DATE: 15-FEB-2000
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-OCT-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy S.
 REGISTRATION NUMBER: 35, 367
 REFERENCE/KEY NUMBER: 016940-00002005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0400
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2995 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 139..2925
 OTHER INFORMATION: /product= "kb"
 /note= "retroblastoma tumor suppressor"
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US 09 860 211 7

Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4777.00 Matches: 925
 Percent Similarity: 99.78% Conservative: 1
 Best Local Similarity: 99.68% Mismatches: 2
 Query Matches: 99.56% Indels: 0
 DB: 10 Gaps: 0

US 09 026 459a 51 (1-928) x us-09-860-211-7 (1-2995)

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455 ArgValMetGluSerMetLeuLysSerGluGluArgLeuSerIleGlnAsnPheSer 474

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RESULT 11
US-09-469-522-32
: Sequence 32, Application US/09469522
: Patent No. US20040151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Xu
: Ho, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US2004/469,522
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: C08A0000
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/026,459
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: UFXL:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3323 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2559
: SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-469-522-32
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Score: 4357.00 Matches: 848
Percent Similarity: 99.88% Mismatches: 1
Best Local Similarity: 99.76% Indels: 0
Query Match: 90.81% Gaps: 0
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PES011 14

US 09-026-459-522-3

Sequence 3, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION

APPLICANT: Xu, Hong Ji

Hu, Shi Xue

Ren, Jie, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-026-459-522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibbert, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UT003506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-9000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2454
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-026-459-522-3

Alignment Scores:

Seq. No.: 0 Length: 3218
Score: 4192.00 Matches: 816
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.47% Indels: 0
DB: 10 Gaps: 0

US-09-026-459A-51 (1-928) x US-09-026-459-522-3 (1-3218)

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 DB 1327 GGTGAACATGGAATCAAGAAAGCTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
 QY 573 IleLysGlnSerLysAspArAllyGlyProThrAspHisLeuGlnSerAlaLysProLeu 592
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 QY 593 AsnLeuProLeuGlnAsnAspHisThrAlaAlaAspMetTyrLeuGlnProValArgSer 612
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QY 613 ProLysLysLysGlySerThrThrArqValAsnSerThrAlaAspAlaGlnGlnGlnGlnGln 632
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 QY 633 ThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheLysLys 652
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RESULT 15
 us-09-026-459a-51-44
 Sequence 44, Application US/09469522
 Patent No. US20020151461A1
 GENERAL INFORMATION:
 APPLICANT Xu, Hong-Ji
 Hu, Shi-Xue
 Benedict, William F.
 Zhou, Yunli


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CY 501 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrPheLeuAsnVal 520
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DB 1174 GTTAAATTTAAAGCTTTTGAATTTTACAAAGTCATGCAAACTTTTATGCAAGCCACAAAGC 1233
CY 581 AsnLeuThrArgGluMetIleLysHisIleuGluArgCysGluHisArgIleMetGluSer 560
DB 1244 AACTTTCANCAANAAATGATAAATATTTAGANCAAGTGGAAATATGAAATCATGAAATTC 1293
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DB 1894 ATGACAGACATCAAAATATAATTTTCCAGTATGCTTCCACCCAGCCGCCCTACCTTGCA 1953
CY 781 ProLeuProHisIleProAlaGlnSerProTyrLysPheProSerSerProLeuArgIlePro 800
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CY 861 ArgSerAlaGluGlySerAspProLeuLysPheLeuLysLysLeuArgPheAspIleGlu 880
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DB 2254 GATCTTATSAAGTATGAAATATAATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2313
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CY 921 AspThrSerAsnLysGluGluLys 928
DB 2374 GATACCTCAAAACAAAGCAAGCAAGAA 2397

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GenCore version 5.1.1.3
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OM nucleic acid sequence search, using SW model

Run on: January 16, 2003, 15:29:22 ; Search time 97.0922 Seconds
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Filter: US 09 026 459A 50

Perfect score: 9554

Sequences: 1 CCGGATGAGGCTGTAAGAC.....AAATGAGGATTAATGATAGT 3554

Scoring table: IDENTITY NP*

Gapop 10.0 ; Gapext 1.0

Searched: 95868 seqs, 222944145 residues

Total number of hits satisfying chosen parameters: 767746

Minimum hit seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4554	100.0	4554	10	US-09-469-522-50 Sequence 50, Appl
2	4550.8	99.9	4555	9	US-09-469-522-1 Sequence 1, Appl
3	4549.8	99.9	4809	9	US-09-954-531-143 Sequence 143, Appl
4	4443.8	96.9	3455	10	US-09-469-522-28 Sequence 28, Appl
5	4379.8	95.1	3392	10	US-09-469-522-30 Sequence 30, Appl
6	4351.6	94.3	3461	10	US-09-469-522-40 Sequence 40, Appl
7	4311.8	93.2	3223	10	US-09-469-522-42 Sequence 42, Appl
8	4253.8	91.5	4256	10	US-09-469-522-34 Sequence 34, Appl
9	4222.8	90.7	3324	10	US-09-469-522-48 Sequence 48, Appl
10	4212	90.4	3218	10	US-09-469-522-4 Sequence 4, Appl
11	4192.4	89.8	3383	10	US-09-469-522-48 Sequence 48, Appl
12	4180.4	89.5	3377	10	US-09-469-522-46 Sequence 46, Appl
13	4126.8	88.0	3487	10	US-09-469-522-42 Sequence 42, Appl
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15	2853.2	80.3	2995	10	US-09-860-211-7 Sequence 7, Appl
16	2827.4	79.6	3181	10	US-09-469-522-44 Sequence 44, Appl
17	428	12.0	451	9	US-09-756-692-7740 Sequence 7740, Ap
18	142.2	4.0	411	10	US-09-864-761-4141 Sequence 3131, Ap
19	129	3.6	129	10	US-09-864-761-1910 Sequence 1910, A

20	104	2.9	304	10	US-09-964-824A-296	Sequence 296, App
21	68.8	1.9	3960	9	US-09-292-758-37	Sequence 37, Appl
22	59.4	1.7	324	9	US-09-796-692-2536	Sequence 2536, Ap
23	51	1.4	3747	10	US-09-770-657-1	Sequence 1, Appl
24	51	1.4	3247	12	US-10-625-626-2	Sequence 2, Appl
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27	48.8	1.4	335913	9	US-09-754-853A-3	Sequence 3, Appl
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33	47	1.3	393	10	US-09-960-352-4582	Sequence 4582, Ap
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35	45.8	1.3	431	10	US-09-960-352-5558	Sequence 5558, Ap
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43	44.2	1.2	1376	10	US-09-976-927A-759	Sequence 749, App
44	44.2	1.2	2000	9	US-09-948-842A-5166	Sequence 5166, App
45	44.2	1.2	3209	10	US-09-220-893-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-469-522-50

Sequence 50, Application US-09469522

Patent No. US23020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: A CELLULAR BINDING AGENT FOR THE CELLULAR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.40

APPLICATION NUMBER: US-09/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: 01X0506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 3554 base pairs

TYPE: nucleic acid

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3542 GGATTTATGATAGT 3554

RESULT 2

US-09-469-522-1
Sequence 1, Application US/99469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UIX0506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:

GenCore version 5.1.3
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oM nucleic acid - nucleic search, using sw model

Run on: January 16, 2003, 15:20:22 : Search time 92.6665 Seconds
(without alignments)
16320.731 Million cell updates/sec

Titles: US-09-026-459A-30

Ported score: 3492

Sequence: 1 GGCAATGAGGATTTTACGGG.....AAATGAGGATTTTACGACT 3392

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 494868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 767746

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3383	99.7	3455	10	US-09-469-522-28 Sequence 28, Appl
3	3383	99.7	3455	10	US-09-469-522-1 Sequence 1, Appl
4	3383	99.7	4839	9	US-09-954-531-143 Sequence 143, App
5	3379.8	99.6	3554	10	US-09-469-522-56 Sequence 50, Appl
6	3315	97.7	3323	10	US-09-469-522-32 Sequence 32, Appl
7	3257	95.9	3265	10	US-09-469-522-34 Sequence 34, Appl
8	3226	95.1	3323	10	US-09-469-522-38 Sequence 38, Appl
9	3225.4	95.1	3461	10	US-09-469-522-40 Sequence 40, Appl
10	3212	94.7	3218	10	US-09-469-522-3 Sequence 3, Appl
11	3167	91.6	3113	10	US-09-469-522-36 Sequence 36, Appl
12	3024.6	89.2	3383	10	US-09-469-522-48 Sequence 48, Appl
13	3012.6	88.8	3377	10	US-09-469-522-46 Sequence 46, Appl
14	3006	88.6	3347	10	US-09-469-522-12 Sequence 42, Appl
15	2827.4	83.4	3161	10	US-09-469-522-44 Sequence 44, Appl
16	2686.4	79.2	2995	10	US-09-860-211-7 Sequence 7, Appl
17	428	12.6	451	9	US-09-796-692-7740 Sequence 7740, Ap
18	142.2	4.2	411	9	US-09-864-761-3141 Sequence 3141, Ap
19	129	3.8	129	10	US-09-864-761-19410 Sequence 19410, A

Sequence 296, App
Sequence 37, Appl
Sequence 2946, Ap
Sequence 1, Appl1
Sequence 2, Appl1
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Sequence 2, Appl1
Sequence 3, Appl1
Sequence 42, App
Sequence 343, App
Sequence 4, Appl1
Sequence 11218, A
Sequence 14721, A
Sequence 4582, Ap
Sequence 154, App
Sequence 5558, Ap
Sequence 11244, A
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Sequence 12358, A
Sequence 2769, Ap
Sequence 4147, Ap
Sequence 4050, Ap
Sequence 749, App
Sequence 5166, Ap
Sequence 4, Appl1

ALIGNMENTS

RESULT 1

US-09-469-522-30
Sequence 30, Application: US/95459522
Patent: No. US20020151461A1

GENERAL INFORMATION

Applicant: Xu, Hong Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4434

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210 4434

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/99/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Hübner, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UIXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 3392 base pairs

TYPE: nucleic acid

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Q7	4138	CAAAAATGATATTATTAACAAATAGAAAAAAATTAATAATTACATTACATTATAT	4197
Db	4069	CAAAAATGCAATTAATCAAAATAGAAAAAAATTAATAATTATACATTATAT	4128
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Db	4189	TAAAGCTGTAAGCAAAATATAAATATATGATATATACATACATAGTACGTAACAAACAGATTTCAT	4248
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Db	4249	AGCTTCAGAAATGTAAGAAAGCTTATGATTAATTTCTGTCATGCACCTATATGTTTTAAATG	4308
Q7	4378	AGGATTAATGATAGT	4392
Db	4309	AGGATTAATGATAGT	4323

THE

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1  US 09 469 522 34
2  Sequence 34, Application US/09469522
3  Patent No. US20020151461A1
4  GENERAL INFORMATION:
5  APPLICANT: XU, Hong-Ji
6  Hu, Shi-Xue
7  Benedict, William F.
8  Zhou, Yunli
9  TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
10 PROTEINS
11 NUMBER OF SEQUENCES: 51
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Arnold, White & Durkee
14 STREET: P.O. Box 4433
15 CITY: Houston
16 STATE: TX
17 COUNTRY: USA
18 ZIP: 77210-4433
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent In Release #1.0, Version #1.30
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/09/469,522
26 FILING DATE: 22-Dec-1999
27 CLASSIFICATION: Unknown
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 09/026,459
30 FILING DATE: Unknown
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Hibler, David W.
33 REGISTRATION NUMBER: 41,071
34 REFERENCE/DOCKET NUMBER: UICX:506
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 512/418-6000
37 TELEFAX: 512/474-7577
38 INFORMATION FOR SEQ ID NO: 34:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 4266 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 FEATURE:
45 NAME/KEY: CDS
46 LOCATION: 7..2502
47 SEQUENCE DESCRIPTION: SEQ ID NO: 34:

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RESULT 9

US-09-469-522-40

: Sequence 40, Application US/09449522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED FFITIN-ELASTOMA TDM-P SUPPRESSOR
: PROTEINS

: NUMBER OF SEQUENCES: 51

: CURRENT SEQUENCE ADDRESS:

REFERENCE/WORKSET NUMBER: DTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418 3000
 TELEFAX: 512/474 7577
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2454
 SEQUENCE DESCRIPTION: SEQ ID NO: 43:

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 Best Local Similarity: 100.0%; Pred. No. 0;
 Matches 4212; Conservation: 0; Mismatches 0; Gaps 0;

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 1747 GAACTCATGAG 1806
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QY 3061 TATATAATTTTCAAGAGCTTCTGAGAGATATATATATTTTACCTGAGAGAGATCA 3120
10 2887 TATATAATTTTCAAGAGCTTCTGAGAGATATATATATTTTACCTGAGAGAGATCA 2946
QY 3121 TATATAATTTTCAAGAGCTTCTGAGAGATATATATATTTTACCTGAGAGAGATCA 3180
10 2947 TATATAATTTTCAAGAGCTTCTGAGAGATATATATATTTTACCTGAGAGAGATCA 3006

QY 3181 TACACATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3240
Db 3007 TACACATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3066
QY 3241 TTTTGGCTTTTAAATATAAATAAAGCTGGAAGCAAGATATAACCAATACATACATACATAC 3300
Db 3067 TTTTGGCTTTTAAATATAAATAAAGCTGGAAGCAAGATATAACCAATACATACATACATAC 3126
QY 3301 ACTGAACACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3360
Db 3127 ACTGAACACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3186
QY 3361 ACTGAACATTTTAAATGAGGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3420
Db 3187 ACTGAACATTTTAAATGAGGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3218
RESULT 11
US-09-469-522-36
Sequence 36, Application: US/09469532
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedit, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SHOUNCHES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4133
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CREATING SYSTEM: PC 255, MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469 522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01XG:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474 7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2349
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-469-522-36
Query Match 91.6%; Score 3107; DB 10; Length 3113;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 286 AGTCACACATTTTGAAGAAGTATGATTTTGTTCACCTCTTCAGCAAAATTCGAAAGG 345

1b	7	ATGTCAGAAAGTGGTGAAGAGTATGATGATTTGTTGGACCTCTTCAGCAAAATTTGGAAGG	66
346	346	AATATGGAATTAATAATATGACACAAACGACAGTGTGCAATGATAGAAATAAATTCCT	405
1b	67	AATGTGAATTTATATATTGTAACAAACGACAGCTTGATATCTACTGAAATATAATTCCT	126
346	406	GATGTTGCTGAAGATTTCTTGATCATCATTTTATTAGCTAAAGGGAGATTTACAA	465
1b	127	GATATGTTGCTAAAGGTTCTTGACATCATTTTATTAGCTAAAGGGAGATTTACAA	186
346	466	ATGCAATGATGATCTGCTGATTTTCATTTTAAATATGCTATGTCGCTGTAATTTTATT	525
1b	187	ATGCAATGATGATCTGCTGATTTTCATTTTAAATATGCTATGTCGCTGTAATTTTATT	246
346	526	AAATTTTCATTTCTCAATGTTGTTGCAAAATCAATAAAACAGTGTGTAATGCAATTAAT	585
1b	247	AAATTTTCATTTCTCAATGTTGTTGCAAAATCAATAAAACAGTGTGTAATGCAATTAAT	306
346	586	GTTTCATCTGGAATACAGACAGAGTGTGAAACAGAGTGTGAAAGTAGTAAACAACTA	645
1b	407	GTTTCATCTGGAATACAGACAGAGTGTGAAACAGAGTGTGAAAGTAGTAAACAACTA	366
346	646	GAAATGATCAAGAATATTATTAATTTCTGTTAAAGAACATGTAATGTATATAGATGAG	705
1b	467	GAAATGATCAAGAATATTATTAATTTCTGTTAAAGAACATGTAATGTATATAGATGAG	426
346	706	GTCAAAAATCTTAATCAAAAAATTTAATCTTTTAATCAATTTCTTGACCTGTGAACA	765
1b	427	GTCAAAAAATCTTTATTCAAAAATTTTATACCTTTTATGAAATCTCTTGACCTGTGAACA	486
346	766	TCTAATGCAATTCAGAGGTTGAAAATCTTTCTTAAAGATACGAGAAATTTATCTTAAA	825
1b	487	TCTAATGCAATTCAGAGGTTGAAAATCTTTCTTAAAGATACGAGAAATTTATCTTAAA	546
346	826	ATAAAGATTCATATGCAAAATTTTGTGGATCATGATAAAATCTTCAATGATCTCT	885
1b	547	ATAAAGATTCATATGCAAAATTTTGTGGATCATGATAAAATCTTCAATGATCTCT	606
346	886	AATATAGTTTGAAGAACAGACAAACACACGAAAAAGTAACTTTGATGACAGAGTCAAT	945
1b	607	AATATAGTTTGAAGAACAGACAAACACACGAAAAAGTAACTTTGATGACAGAGTCAAT	666
346	946	GTAAATCTCTCAACACTCTGTTAGAGATCTGTTGACACATCTCCACCAATTAATGATG	1005
1b	667	GTAAATCTCTCAACACTCTGTTAGAGATCTGTTGACACATCTCCACCAATTAATGATG	726
346	1006	ATTTTAAATTCACAAATGATCAAAATTCAGAAAAATGATTTCTATTTAAACATGTC	1065
1b	727	ATTTTAAATTCACAAATGATCAAAATTCAGAAAAATGATTTCTATTTAAACATGTC	786
346	1066	ACATGCAATGCAAAATGAAATATATGCAAAAGATGACAGATATAGGATATCTTTAAA	1125
1b	787	ACATGCAATGCAAAATGAAATATATGCAAAAGATGACAGATATAGGATATCTTTAAA	846
346	1126	GAAATTTCTGAAATCTGTGGACAGGCTTGTGTGAAATTTGATCATACAGATACAAA	1185
1b	847	GAAATTTCTGAAATCTGTGGACAGGCTTGTGTGAAATTTGATCATACAGATACAAA	906
346	1186	CTTGAATGCTGATTTGATTAATGAGTAATGGAATTCATGCTTAAATCAGAGAGAACGA	1245
1b	907	CTTGAATGCTGATTTGATTAATGAGTAATGGAATTCATGCTTAAATCAGAGAGAACGA	966
346	1246	TATATATATCAAAAAATTAATCAAACTCTGGAATGCAATTTTCAATCTTTATTC	1305
1b	967	TATATATATCAAAAAATTAATCAAACTCTGGAATGCAATTTTCAATCTTTATTC	1026
346	1306	GATGTTGCTGTTGAGGTTGTAATGAGGATAATAGCAAGATATATCTGAAATCTTGAT	1365
1b	1027	GATGTTGCTGTTGAGGTTGTAATGAGGATAATAGCAAGATATATCTGAAATCTTGAT	1086
346	1366	TCTGGAATCAATTTGCTTTGCAATGATCTGAAATGCTTAAATTTAAAGGCTTTGAT	1425

1087 TCTGGACAGAGATTGTGCTTTCCCATGAGATTCTGATGTGTTAAATTTAAAAAGCTTTGAT 1144

1426 TTTTACAAAGTCATCGAAAGCTTTATCAAGAGCAAGAGCAAACTTTCACAGAGAATAACATGATA 1485

1147 TTTTACAAAGTCATCGAAAGCTTTTATCAAGAGCAAGAGCAAACTTTCACAGAGAATAACATGATA 1206

1486 AATATTATTGAGCATGTGAGCATCGAATTCATGAGTAATCGCTTTGATGTGTTATCTTCATATTTCA 1545

1207 AATCATTTTACAAAGCATGTGAGCATCGAATTCATGAGTAATCGCTTTGATGTGTTATCTTCATATTTCA 1266

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1267 CATTATTTGATGCTTATTAACCAATCTAAAGAGATCAAGAGAGAGCAATCAATCTACATCACTTCGAA 1326

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1327 TCTGCTGTGTCCTCTTAACTCTTCCCTCTTCAGATAAATATCACTCTGAGCAATATATATGATGATCTT 1386

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1387 TCTGCTGTGATGATCTCTCAAGAGAAAAAGATCTCAATTAGCGGTGTAATTTCTTACTCTCAAAAT 1446

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1507 TCACCTGTTTATAAAAAAGTCTATCGCTAGCTCTATCTCCGCTTAAATACATCTTCTTCGAA 1566

1846 GAGCTTCTGCTGAGAGCAAGAAATTAGAACATATCATCTGGAGAGCTTTCTCCAGCAATAC 1905

1567 GAGCTTCTGCTGAGAGCAAGAAATTAGAACATATCATCTGGAGAGCTTTCTCCAGCAATAC 1626

1906 CTTGAGAGATGACTATGAACTCATCAGACATCAGACATACAGCAATCTTCCAGCAATCTTCTTCG 1965

1627 CTTGAGAGATGACTATGAACTCATCAGACATCAGACATCTTCCAGCAATCTTCTTCGAGCTTCTTC 1686

1966 ATGTATGCCATATGCCAAGTCAAGCAATATAGATCTTAAATCTTAAATCTTCTTCAATCAATCA 2025

1687 ATGTATGCCATATGCCAAGTCAAGCAATATAGATCTTAAATCTTAAATCTTCTTCAATCAATCA 1746

2026 TACAAAGATCTTCTCATGTGTTGTCAGAGAGCAATCTCAAAAGTCTTTTCTATCTCAAAAGAG 2085

1747 TACAAGGATCTTCTCATGTGTTGTCAGAGAGCAATCTCAAAAGTCTTTTCTATCTCAAAAGAG 1806

2086 CAGATGATCTTCTATTTAGTATCTCTAATCTGCTCTTCACTGAGAGATCTGAGAGATCTGAGAGAT 2145

1807 GAGTATGATCTTCTATTTAGTATCTCTAATCTGCTCTTCACTGAGAGATCTGAGAGATCTGAGAGAT 1866

2146 ATTCTGCACTATGCTTCCATGAGGCTGCTGAGGATCTGCTGATCAATCAATCAATCTTCTTCTGCA 2205

1867 ATTCTGCACTATGCTTCCATGAGGCTGCTGAGGATCTGCTGATCAATCAATCAATCTTCTTCTGCA 1926

2206 AGCTGTTAAAGTTTCTATTTAGTATCTCTAATCTGCTCTTCACTGAGAGATCTGAGAGATCTGAGAGAT 2265

1927 AGCTGTTACAGTCTTCTGATGAGGATCTGAGGATCTGAGGATCTGAGGATCTGAGGATCTGAGGAT 1986

2266 CCGCTCAAGACTGCTATATAAAATTTTCAGAGAGCTTCTGATCAATCAATCAATCAATCTTCTGCA 2325

1987 CCGCTGAGAGCTGCTATATAAAATTTTCAGAGAGCTTCTGATCAATCAATCAATCAATCTTCTGCA 2046

2326 AGATCAAGCAATCTTATGATCTAAATTTGCTGATCAATCTGAGGATCTTCTGATCAATCAATCAAT 2385

2047 AGATCAAGCAATCTTATGATCTAAATTTGCTGATCAATCTGAGGATCTTCTGATCAATCAATCAAT 2106

2386 ATAATCATGATGATGTAATCAAGAGATCTGATGATCTGATGATCTGATGATCTGATGATCTGATGAT 2445

2107 ATAATCAGATGGTATCTAACAGAGATCTGATGATCTGATGATCTGATGATCTGATGATCTGATGAT 2166

2446 CCGCTCAAGACTGCTATATAAAATTTTCAGAGAGCTTCTGATCAATCAATCAATCAATCTTCTGCA 2505

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[illegible]

2755 GATGCAATTTTGGTTCATTGTAAGCCACCTGAAATGTTATCATTTTATTATACA 2814
QY 2840 ACATTCAGAAATCTCTGTAATCTCCGCAATTAATAAGTCTGACCATGTTCTCTCT 2889
DB 2815 AATTTGAAATCTCTGTAATCTCCGCAATTAATAAGTCTGACCATGTTCTCTCT 2874
QY 2890 CCAAAAGTAAATCTCTGTTATGATAGTAAGTAAATCTCTGTTATGATAGTAAG 2949
DB 2875 CCAAAAGTAAATCTCTGTTATGATAGTAAGTAAATCTCTGTTATGATAGTAAG 2934
QY 2900 TAAAGCAGGCTGCTGATCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3009
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QY 3010 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3069
DB 2995 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3054
QY 3070 GTCCTGATCTCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3129
DB 3055 GTCCTGATCTCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3114
QY 3130 GTCCTGATCTCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3189
DB 3115 GTCCTGATCTCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3174
QY 3140 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3249
DB 3175 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3234
QY 3250 TAAITTAATAAAGCTGAGCAAAATATAATTAATTAATTAATTAATTAATTAATTAAT 3309
DB 3235 TAAITTAATAAAGCTGAGCAAAATATAATTAATTAATTAATTAATTAATTAATTAAT 3294
QY 3310 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3369
DB 3295 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3354
QY 3370 TTTAAAGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3392
DB 3355 TTTAAAGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3377

RESUB 14
US 09 469 522-42
Sequence 42 App'd for Sec. 102/2994/9522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
Hu, Shi Xue
Benedit, William P.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOLACT-MA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CURRENT INVENTOR: ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent for P-1-asp #1 0, V-1-asp #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: 06060606
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 7..2583
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-469-522-42
Query Match 88.6%; Score 3096; DB 10; Length 3347;
Best Local Similarity 100.0%; Pred No 0;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 387 ATTACTGAAATAAAATTTGTTTGTGTTTAAAGTTTGTGATACATTTTATTATAG 446
DB 342 ATCTACTGAAATAAAATTTGTTTGTGTTTAAAGTTTGTGATACATTTTATTATAG 401
QY 447 TAAAGGAGATATTAATAAGGAGATGATGTTGTTGATTTCAATTCATTAATGTTATG 506
DB 402 TAAAGGAGATATTAATAAGGAGATGATGTTGTTGATTTCAATTCATTAATGTTATG 461
QY 507 TGTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 566
DB 452 TGTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 521
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QY 627 AGTTGTTGATTAATAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 686
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QY 747 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 806
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QY 807 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 866
DB 762 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 821
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DB 822 AACTTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 881
QY 927 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 986
DB 882 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 941
QY 987 TATCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 1046
DB 942 TATCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 1001
QY 1047 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 1106
DB 1002 TTTCTTGGATTTGTTTAAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 1061



Percent Similarity: 99.89%	Conservative: 0
Best local Similarity: 99.89%	Mismatches: 1
Query Match: 99.67%	Indels: 0
Indel: 10	Gaps: 0
00: 99 026 459a 29 (1 895) x 95 99 860 211 7 (1 2995)	
QY 2	GluAspSerGlyProGluAspGluProLeuValArgLeuGluPheGluThrGluGlu 21
DB	1201 AGACACCCAGCAAAAAGAAAGCAAGCTTCATCAGACAGCGTGAAGTAAATCTTCACACACACACAC 1260
QY 22	ProAspPheThrAlaLeuGlyCysGlnLysLeuLysIleProAspPheLysValArgGluArgAla 41
DB	342 ValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAsp 461
QY 301	CysGln 360
DB	1261 GTTAGGACTGTATGACACATCCACAAATTAATGATGATTTTAAATTCAGTAAGTGAT 1420
QY 42	TrpLeuThrTrpGlnLysValSerSerValAspGlyValLeuGlyGlyTyrIleGlnLys 61
DB	362 GlnProSerGluAsnLeuIleSerTyrPheAsnAspCysThrValAsnProLysGluSer 381
QY 361	0351 AAACGACAGAACTTCACTGCGGATCGGACGATGGAGGTATATATCAAAAAG 420
DB	1321 CAACCTTCAGAAAATCTGATTTCCATTATTTAACTACACACACACACACACACACACACAC 1480
QY 62	LysLysGlnLeuTrpGlyIleCysIlePheIleAlaValAspLeuAspGluMetSer 81
DB	382 IleLeuLysArgValLysAspIleGlyTyrIlePheLysGlnLysPheAlaLysAlaVal 401
QY 421	AAAAAGAACTGTGGGAAATCTGATTTTATTTGACAGCTTACCTAGATGAGATGCG 480
DB	1381 ATACTCAAAAGACAGTGAAGCAATACAGATACAGATTTAAAGAGAAAATGCTTAAAGCTGCT 1440
QY 82	PheThrPheThrGlnLeuGlnLysAsnIleGlnIleSerValHisLysPhePheAsnLeu 101
DB	402 GlyGlnGlyCysValGlnIleGlySerGlnArgTyrGlyLysLeuGlyValAsnAlaSer 421
QY 481	PICACTTTTACAGCTACAGAAAACATAGAAAATCAGTGCCATATAATCTTTAACTTAA 540
DB	1441 GGCAGGGTTGTGTGGAATTTGGATCAGACGATACAAATTTGAGGTTCCTTTGATTATC 1500
QY 102	LeuLysGlnIleLeuAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLys 121
DB	422 ArgValMetGlnSerMetLeuLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 441
QY 541	CTAAAGAAATTCATACAGTACAAAGCTTCAATGCTATGCTACAGACCTTCAAGAAC 600
DB	1501 CGATTAATGGAATCATGCTTAAATTCAGAAAGAAAGGATATCATCAATCAAAAATTTTACG 1560
QY 122	TyrAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGlnLeuIleTyrLeu 141
DB	442 LysLeuLeuAsnAspAsnIlePheIleSMetSerLeuLeuAlaCysAlaLeuGlnAlaVal 461
QY 601	TATGATGTAATTTGATGAACTTCAAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 660
DB	1561 AAACCTTCGAATGACAAACATTTTCAATAGCTTTATTCGGCTGCTCTTGAGCTTCTA 1620
QY 142	ThrGlnProSerSerIleSerThrGlnIleAsnSerAlaLeuValLeuLysValSer 161
DB	462 MetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhe 481
QY 661	ATACAAACCCAGCAGTTCGATATCTACGCAAAATTAATTTCTGCTTGGTTCGCTTAAAG 720
DB	1621 ATGGCCACATATAGCAGAAAGTACATCTCAGAAATCTGATTTCTGACACAGATTTCTCTTC 1680
QY 162	TrpIleThrPheLeuLeuAlaLysGlyGlnValLeuGlnMetGluAspAspLeuValIle 181
DB	482 ProTrpIleLeuAsnValIleAsnLeuLysAlaPheAspPheTyrLysValIleGluSer 501
QY 721	TCATACACATTTTATTAAGTAAAGCTTAAATTTAAAGGCTTTGATTTTAAAGTGAATG 1740
DB	1681 CGATGGATTTCTGAATGCTTAAATTTAAAGGCTTTGATTTTAAAGTGAATGGAAGT 1740
QY 182	SerPheGlnLeuMetLeuGlyValLeuGlyAspTyrIleLysLeuSerTrpProMetLeu 201
DB	502 PheIleLysAlaGlnGlyAspLeuThrArgGlnMetIleCysPheLysLeuGlnArgCysAla 521
QY 781	TCATTTCAATTAATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB	1741 TTTATCAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1800
QY 202	LeuLysGlnProGlyTyrThrAlaValIleProIleAspGlySerProArgThrProArg 221
DB	522 HisArgIleMetGlnSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLys 541
QY 841	CTCAAGAACATATAAAACACCTGCTATACCCATTAATGCTTACCTTCAAACTCCAG 900
DB	1801 CATCAATCATGTAATGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 222	ArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIle 241
DB	542 GlnSerLysAspArgGlnGlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeu 561
QY 901	CGAGTTCACAAACAGAGTCAAGATACGATACGATACGATACGATACGATACGATACGAT 960
DB	1861 CAATCAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1920
QY 242	GluValLeuGlySerLeuHisSerCysAsnIleAspGlnValLysAsnValTyrPheLys 261
DB	562 ProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLys 581
QY 961	GAGGTTCCTGTAAGAACATCAAGATGATATAGATGAGGTGAAAAAGTTATTTTCAAA 1020
DB	1921 CCTCTCCACAAATATACACATCCACACACACACACACACACACACACACACACACAC 1980
QY 262	AspPheIleProPheMetAsnSerLeuGlyLysValThrSerAsnGlyLeuProGlnVal 281
DB	601 LysLysGlySerThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 601
QY 1021	AAATTTATACCTTTTATCAAACTCTCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 1080
DB	1981 AAAAAAGTTCAAATACGCGTGAATTTCTATGTAAGTGAATTTCTATGTTTATATAAAAAAG 2040
QY 282	GluAsnLeuSerLysArgTyrGlnIleTyrLeuLysAsnLysAspLeuAspAlaArg 301
DB	2041 GCTTCTCAAGAAAGGACATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2100
QY 1081	GAATAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB	622 TyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyAsnAlaArgLeuLeuSerGlnHisPro 641
QY 302	LeuPheLeuAspHisLeuAspGlnIleMetMetCysSerMetTyrGlyTyrIleCysLysVal 681
DB	2101 TATCGGCTAGCCCTATCTCCGGCTAAAATACACTTCTCAAACTGCTGCTGCTGCTGCTGCT 2160
QY 1141	TTATTTTGGATCATGATTAAGAACTCTTCAAGATCTGATCTATAGAAAGTTTTTGAAGAAC 1200
DB	642 GluLeuGlnHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlnTyrGlnLeu 661
QY 322	ArgThrProArgLysSerAsnLeuAspGlnValAsnValIleProProHisThrPro 341
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NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Altabid, Willie & Dukker
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4434

MEDIA READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcutin Release #1 0. V.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-469,522
FILING DATE: 22-Dec-1994
CLASSIFICATION: unknown

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: unknown

ATTORNEY/AGENT INFORMATION:
NAME: Hilder, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DCKET NUMBER: UIXC:506

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURES:
NAME/KEY: CDS
LOCATION: 7..2628
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-469,522-30

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RESULT 12
US 09 469 522-38
Sequence ID: Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RGS IN BRAIN: MA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210 4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01X0506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 3423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 7..2559
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-469-522-38
Alignment Scores:
Pred. No.: 0 Length: 4424
Score: 4217.00 Matches: 821
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0

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Q7 775 ProGluLysSerProTrpLysIleSerArgGlnGlyLeuProSerThrPheSerThrPro 794

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1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

2. The second part of the document is a list of the topics that were discussed at the meeting. The topics are listed in alphabetical order.

3. The third part of the document is a list of the actions that were taken at the meeting. The actions are listed in alphabetical order.

4. The fourth part of the document is a list of the decisions that were made at the meeting. The decisions are listed in alphabetical order.

5. The fifth part of the document is a list of the recommendations that were made at the meeting. The recommendations are listed in alphabetical order.

GenCore version 5.1.3
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conclusions, multiple search, using SW model

from on: January 16, 2007, 15:20:22; Search time: 94.4876 seconds
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US 09 026 459A 28

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Maximum Match 1008

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Printed, N_{pi} is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Best local similarity 100.0%; Pred. No. 0;
Matches 3447; conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GAGGACAGCGCGCGGAGGAGCTGGCTCTGGCAGGCTTGAGTTCAAGAAACAGAGCA 68
DB 108 GCGAGCAAGCGCGCGGAGGAGCTGGCTCTGGCAGGCTTGAGTTCAAGAAACAGAGCA 167

QY 69 AATTCATTTTACAGCAATTAAGTACAGAAATTAAGATACCAGATCATGTCAGAGAGAGC 128
DB 108 AATTCATTTTACAGCAATTAAGTACAGAAATTAAGATACCAGATCATGTCAGAGAGAGC 227

QY 129 TGGTAAATTTGGGAGAAATTTCACTGTGGGATGGAGTATGGGAGGTATATATTCAGAA 188
DB 228 TGGTAAATTTGGGAGAAATTTCACTGTGGGATGGAGTATGGGAGGTATATATTCAGAA 387

QY 189 GAAAAAGAAACGTGGGAAATTCATTTTATGGCAGCAGTGGAGCTAGATGATGTC 248
DB 288 GAAAAAGAAATTCATTTTATGGGAAATTTCACTGTGGGATGGAGTATGGGAGGTATATATTC 347

QY 249 GTTCACATTTTACTGAGCTAGAGAAACATAGAAATCAGTGTCCATAAATTCATTTAAC 308
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DB 468 ATATGATGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 527

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DB 1248 TATACTGAAAGAGCTGAGGATATAGGATATATAGGATATATAGGATATATAGGATATATAG 1307

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DB 1428 CAACCTTCGAAATTCAG 1487

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QY 1449 CCAATGGAATTCGAAATTCAG 1508
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RESULTS

REF: 011 1 5
ISS: 011 461 522 311

US/04469522

; Patent No. US20020151461A1

; FILE NO. 03200201314
; GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

何, Shi-Xue

Benedict, William F.

THE UNIVERSITY OF MICHIGAN LIBRARY

```

1 PROTEINS
2
3 NUMBER OF SEQUENCES: 51
4
5 CORRESPONDENCE ADDRESS:
6
7 ADDRESSEE: Arnold, White & Barker
8
9 STREET: P.O. Box 4433
10
11 CITY: Houston
12
13 STATE: TX
14
15 COUNTRY: USA
16
17 ZIP: 77210-4433
18
19 COMPUTER READABLE FORM:
20
21 MEDIUM TYPE: Floppy disk
22
23 COMPUTER: IBM PC compatible
24
25 OPERATING SYSTEM: PC-DOS/MS DOS
26
27 SOFTWARE: Patent in release #1-0, V
28
29 CURRENT APPLICATION DATA:
30
31 APPLICATION NUMBER: US/09/469,522
32
33 FILING DATE: 22 Dec 1999
34
35 CLASSIFICATION: <Unknown>
36
37 PRIORITY APPLICATION DATA:
38
39 APPLICATION NUMBER: 09/026,459
40
41 FILING DATE: <Unknown>
42
43 ATTORNEY/AGENT INFORMATION:
44
45 NAME: Hibler, David W.
46
47 REGISTRATION NUMBER: 41,071
48
49 REFERENCE/DOCKET NUMBER: 01XC:506
50
51 TELECOMMUNICATION INFORMATION:
52
53 TELEPHONE: 512/438-4000
54
55 TELEFAX: 512/474-7577
56
57 INFORMATION FOR SEQ ID NO: 40:
58
59     SEQUENCE CHARACTERISTICS:
60
61         LENGTH: 3492 base pairs
62
63         TYPE: nucleic acid
64
65         STRANDEDNESS: single
66
67         TOPOLOGY: linear
68
69     FEATURE:
70
71         NAME/KEY: CDS
72
73         LOCATION: 7..2628
74
75         SEQUENCE DESCRIPTION: SEQ ID NO: 40:
76
77     GS-09-469-522-30

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Query Match:	97.4%	Score 4983	Lib 13	Length 4422
Best Local Similarity	100.0%	pred. No. 0		
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Db	10	GATTTTACTGCTATTATGTCAGAAATTAAGATATACAGATATGTCAGAGACAGAGCTTGG	69	
QY	133	TTAACTTGGGACAAAGTTTCATCTGTCGGAACGAGTATTCGACGATTCGACGATTCGACG	192	
Db	70	TTAACTTGGGACAAAGTTTCATCTGTCGGAATGAGTATTCGACGATTCGACGATTCGACG	129	
QY	193	AAGGAACCTGTGGGCAATCTGATCTTTATTTGTCAGAGTTGATCTASATGATGCTGTC	252	
Db	130	AAGGAACCTGTGGGCAATCTGATCTTTATTTGTCAGAGTTGATCTASATGATGCTGTC	189	
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QY	373	GATGATTTGTTTGCACCTCTTCAGCAAAATGCAAGACATGTCGAACCTATATAATTTGAA	432	
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QY	433	CACCAACAGAGTTTGATATCTATGAAATTAATCTGATCTGCTCTCTAAAGTTTCTTGG	492	
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Db 2530 AATATAGAGAT 2589
QY 2653 AATATAGAGAT 2712
Db 2590 AATATAGAGAT 2649

Sequence 4, Application US/9446522
 Patent No. US2003011461A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong Ji
 80, Shi Xue
 Benedict, William F.
 Zhou, Yunli
 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Porro
 STREET: P.O. Box 4443
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210 4443
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/9446522
 FILING DATE: 22 Dec 1999
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: Unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Hubler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/WORK NUMBER: UIC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/414 3000
 TELEFAX: 512/474 7577
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3218 base pairs
 TYPE: nucleotide acid
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 TOPOLOGY: linear
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 NAME: KEY_CTS
 LOCATION: 7..2474
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US 09 469 522 3

Query Match
 Best Local Similarity 100.0% Pred. No. 0;
 Matches 3212: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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us protein nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 04:31:54, Search time: 67.7443 seconds
(without alignments)
6107.852 million cell updates/sec

Filter: US-09-026-459A-2

Perfect score: 4797

Sequences: 1 MPKTRKTAATAAAAAAEP.....TRMKKMDMSMTSKKEK 928

Scoring table:

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Gapop 10.0, Xgapext 0.5
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Scorched: 99868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787735

Minimum db seq length: 0

Maximum db seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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us-09-026-459A-2

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RESULT 7

US-09-459-522-30

Sequence 30, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

In, Shi Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED REINBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Lippke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patout In Release #1.0, Version #1 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09-026-459

FILING DATE: 22 Dec-1999

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09-026-459

FILING DATE: unknown

ATTORNEY/AGENT INFORMATION:

NAME: Bibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DECKET NUMBER: 01XC:506

TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 3392 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2628

SEQUENCE DESCRIPTION: Seq ID NO: 30-

us-09-026-459a-2

us-09-026-459a-2 (1-928) x us-09-459-522-30 (1-3392)

Alignment Scores:

Prod. No.: 0 Length: 3392

Score: 4499.00 Matches: 873

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 94.79% Indels: 0

Gaps: 0

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167b	1670	TTTCAGACGTCACAGACCAATCGAAATACCGCTCTTCTACTGTTTATAAAAAAGTCTAT	1809
168b	1680	CGGTTACATCTCGGATCGGAGTAATATACNTTGTCAACGCTCTGTCTGACACCCAGAA	1869
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221b			

Hu, Shi Xue
 Benedict, William F.
 Zhou, Yunli
 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Burke
 STREET: P.O. Box 4434
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210 4434
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/067,459, 622
 FILING DATE: 22 Dec 1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hiblet, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UICX-506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3377 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2613
 SEQUENCE DESCRIPTION: SEQ ID NO: 46:
 GS-09_469-522-46

RESULT B
 US 09 469 522 46
 : Sequence 46, Application, US/09469522
 : Patent No. US200201461A1
 : GENERAL INFORMATION:
 APPLICANT: Xu, Hong Ji

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461 1edlssscGchbclhclgArqLeuSerllecAspPheSerLysLeuLeuAspAsn 480
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14 736 TAGAAGAAATTTATCTTAAAAATAAGATCTAGATGCAATATTATTTGGATCATGAT 795
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QY 461 AsnLeuAspGlnGluValAsnValIleProProIleThrProValAlaGlnThrValMetAsn 380
DB 856 AAATCTTGAAGAAGATGAAATGAAATGCTGACACACATGACGTTAGGACATGTTATCAAC 915
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QY 621 ArqValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
DB 1636 GGTGTAAATCTTATGTAATGCAAGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1695
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QY 661 ArqLeuAsnThrLeuLysGlnArqLeuLeuSerGlnLysProGlnLeuGlnLysIleIle 680
DB 1756 GGGTAAATTAATGATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCT 1815
QY 681 TrpThrLeuPheGlnLysThrLeuGlnAsnGlnTyrGlnLeuMetArqAspArqLysLeu 700

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DB 1876 GACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1935
QY 721 PheLysIleIleValThrAlaTyrLysAspPheProHisAlaValGlnGlnThrPheLys 740
DB 1936 TTCAAAAATCATTTGTAACAGCAATCAAGAGATCTCTCTATGATGATGATGATGATGAT 1995
QY 741 ArqValLeuIleLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 760
DB 1996 CGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2055
QY 761 MetGlnArqLeuLysIleAsnIleLeuGlnIleAlaSerThrArqProIleThrLeuSer 780
DB 2056 ATCCAC 2115
QY 781 ProIleProIleIleProArqSerProTyrLysPheProSerSerProLeuArqIlePro 800
DB 2116 CCAATACCTTCATCT 2175
QY 801 GlyGlyAsnIleTyrIleSerProLysSerProTyrLysIleSerGlnGlnGlnGlnGln 820
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DB 2356 AAAAAATGATGAG 2415
QY 881 GlySerAspGlnAlaAspGlySerLysHisLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 900
DB 2416 GATCAGATGAG 2475
QY 901 LeuAlaGlnMetThrSerThrArqThrArqMetGlnGlnGlnGlnGlnGlnGlnGlnGln 920
DB 2476 CTGGAG 2535
QY 921 AspThrSerAsnLysGlnGlnLys 928
DB 2536 GATATCTCAAAATCAAG 2595
RESULT 13
US-09-469-522-34
Sequence 34, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

QY 481 IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 500
DB 481 ILEPHEHISMETSERLEULEUALACYSALALEUGLUVALLVALLMETALATHRTYRSERARG 500
14 1354 ATTTTCAATATGCTTTTATGAGGAGGAGGCTTTTAAATATTAATAGGCAATATATAGAGA 1113
QY 501 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleLeuAsnVal 520
DB 501 SERTHRSERGINASNLEUASPSERGLYTHRASPLEUSERPHEPROILELEUASNVAL 520
14 1314 AGTACATCTCAGAACTCTTGATTTGATTTGCAACACATATTTCTCTTTTCCCAUGGATTCGAAATG 1173
QY 541 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 540
DB 541 LEUASNLEULYSALA-PHEASP-PHE-TYR-LYS-VAL-ILEGLUSERPHEILELYSALAGLUGLY 540
14 1294 CTTAAATTTAAAGAGCTTTGATTTTACAAAGCAAGCAAGCAAGCTTTTATCAAAAGCAGAGGC 1233
QY 561 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 560
DB 561 ASNLEUTHRARGGLUMETILELYSHISLEUGLUARGCYSGLUHISARGILEMETGLUSER 560
14 1244 AACTTGA-AAAGAAATGATTAATAAATTTTAAAGAGGATGTGAATATGAAATCATGAAATGC 1293
QY 581 LeuAlaIlePheLeuSerProLeuPheAspLeuIleLysGlnSerIleLysAspArgGlu 580
DB 581 LEUALAILEPHELEUSERPROLEUPHEASPLEUILELYSGLINSERILELYSASPARGLU 580
14 1294 CTTCGTAAGGCTTCAGATTCACCTTTATTTGATCTTTATTAACCAATCAAAAGCACCAGAA 1353
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DB 581 GLYPROTHRASP-HISLEUGLUSERALACYS-PROLEUASNLEUPROLEUGLUASN-HIS 600
14 1354 GCAATAACTGATGACCTTGAATCTGCTTGCTTAACTCTTAACTCTCTCCAGAAATAATCAC 1413
QY 621 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySerThrThr 620
DB 621 THRALAALASP-MET-TYR-LEUSER-PROVAL-ARGSER-PRO-LYS-LYS-GLY-SER-THR-THR 620
14 1414 ACTGAAAGATATATATCTTTTCTGTAAAGATCTCCAAAGAAAGAAAGGTTCAACTAGC 1473
QY 621 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaIlePheGlnThrGlnLys 640
DB 621 ARGVALASNSERTHRALAASNALAGLUTHRGINALA-THR-SER-ALA-ILE-PHEGLNTHRGLNLYS 640
14 1474 GGGTAAATATCTTAACTGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1533
QY 641 ProLeuLysSerThrSerLeuSerLeuPheThrValLeuSerGlnHisProGluArgHisThrLeu 660
DB 641 PROLEULYSSERTHRSERLSEULEUPHE-THR-VAL-LEUSERGLNHISPROGLUARGHIS-THRLEU 660
14 1534 GCAATGAAATCTACCTCTCTTCACTTTTATTAATAAGTGTATCGGCTAGGCTATCTC 1593
QY 661 ArgLeuAsnThrLeuCysGluAlaThrLeuGluAsnGluThrValLeuArgLeuAlaThrLeu 660
DB 661 ARGLEUASNTHRLEUCYSGLUALA-THR-LEUGLUASNGLU-THR-VAL-LEU-ARGLEUALA-THRLEU 660
14 1594 GGGTAAATATCTTGAAGAGTCTTCTGCTTAAAGCAGCAAGCAAGCAAGCAAGCAAGCAAG 1653
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DB 681 ARG-PHELEUPHEGLNHIS-THRLEUGLUASNGLU-THR-VAL-LEU-MET-ARG-ASP-ARGHISLEU 700
14 1654 TGGATGTTTTCACAGCACACCTCTGACAACTGAGTATGAACTGATGAGACACAGGCAATTG 1713
QY 701 AspinIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 720
DB 701 ASPINILEMET-MET-CYS-SER-MET-TYRGLYILECYS-LYS-VAL-LYS-ASNILEASP-LEULYS 720
14 1714 GAAATAAATTAAGATGAGTTCAGTATGCGGATATGCGGATATGCGGATATGCGGATATGCGG 1773
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14 1774 TTCAAAATCATCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1833
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14 1834 GGGTAAATATCTTGAAGAGTCTTCTGCTTAAAGCAGCAAGCAAGCAAGCAAGCAAGCAAG 1893
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14 1894 AAGTACAGACAGCAAAACAAATATTTCCAGTATGCTTCCAGCAGGCGCCCTACCTTGCA 1953
QY 781 ProIleProHisIleCysArgSerProTyrLysPheProSerProLeuArgIlePro 800
DB 781 PROILEPROHISILECYS-ARGSER-PRO-TYR-LYS-PHE-PRO-SER-PROLEU-ARGILEPRO 800
14 1954 GCAATATCTCATCTGAGAGGAGTAAAGATTTTATGCTTAACTTAACTTAACTTAACTTAACT 2013
QY 821 GlyLysAsnIleThrLeuSerProLysSerProTyrLysIleSerGluGlyLeuPro 820
DB 821 GLYLYSASNILETHRLEUSERPRO-LYS-SER-PRO-TYR-LYS-ILE-SERGLUGLYLEUPRO 820
14 2014 GCAAGGAACAICATATATTCACCCGCAAGAGTCCATATAAAATTTCAAGAGGTCTGCCA 2073
QY 841 ThrThrThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly 840
DB 841 THRTHRTHR-LYS-MET-THR-PRO-ARG-SER-ARG-ILELEU-VAL-SERILEGLYGLUSERPHEGLY 840
14 2074 AATAAACAACAAAAAGACATCCAGAAATTAAGAAATCTTAACTTAACTTAACTTAACTTAACT 2133

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DB 841 THRSERGLUARG-PHEGLNLYSILEASNGLN-MET-VAL-CYS-ASN-SER-ASP-ARG-VALLEULYS 860
14 2134 ACTTCTGAGAAATTCAGAGAAATAAATCAGATGATGATGATGATGATGATGATGATGATGATGAT 2193
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14 2194 ACAAGTCTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2253
QY 881 GlySerAspGluAlaAspGlySerIleSerProGlyGluSerLysPheGlnIleLys 900
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14 2254 GATTCATATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2313
QY 901 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspAspSerMet 920
DB 901 LEUALAGLUMET-THR-SER-THR-ARG-THR-ARG-METGLNLYSGLNLYS-MET-ASP-ASP-SER-MET 920
14 2314 CTGGCAAAATGCTTCTTATCTCAATACAGAAATGCAAAATGCAAAATGCAAAATGCAAAATG 2373
QY 921 AspThrSerAsnGlyGluGluLys 928
DB 921 ASPTHRSERSNGLYGLUGLULYS 928
14 2374 GATACCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2397

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Job time : 170.743 secs

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us-09-026-459a-34.rnpl

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January 16, 2003, 15:20:22 : Search time 59.2243 seconds
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16420.741 Million cell updates/sec

us-09-026-459a-34

us-09-026-459a-34
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Gapex 10.0, Gapext 1.0

Searches: 99488 seqs, 22294149 residues 787746

Total number of hits satisfying chosen parameters: 787746

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: us-09-026-459a-34
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- 12: us-09-026-459a-34
- 13: us-09-026-459a-34
- 14: us-09-026-459a-34

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4257	99.7	4324	10	us-09-469-522-32
3	4257	99.7	4392	10	us-09-469-522-30
4	4257	99.7	4455	10	us-09-469-522-28
5	4257	99.7	4555	10	us-09-469-522-1
6	4257	99.7	4839	9	us-09-954-531-143
7	4257	99.6	4554	10	us-09-469-522-50
8	4226	99.8	4324	10	us-09-469-522-38
9	4225	99.8	4461	10	us-09-469-522-40
10	4212	99.5	4218	10	us-09-469-522-3
11	4107	99.1	4113	10	us-09-469-522-36
12	4098	92.0	4447	10	us-09-469-522-42
13	2898.6	88.8	3383	10	us-09-469-522-48
14	2898.6	88.4	3377	10	us-09-469-522-46
15	2827.4	86.6	3161	10	us-09-469-522-44
16	2560.4	78.4	2995	10	us-09-860-211-7
17	428	13.1	451	9	us-09-746-692-7740
18	142.2	4.4	411	10	us-09-864-761-3141
19	129	3.9	129	10	us-09-864-761-19910

Sequence 296, Ap
Sequence 37, Appl
Sequence 2546, Ap
Sequence 1, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 342, Ap
Sequence 34, Ap
Sequence 4, Appl
Sequence 11218, A
Sequence 14521, A
Sequence 4582, Ap
Sequence 154, Ap
Sequence 5558, Ap
Sequence 11244, A
Sequence 5785, Ap
Sequence 1, Appl
Sequence 12458, A
Sequence 2769, Ap
Sequence 4147, Ap
Sequence 4050, Ap
Sequence 749, Ap
Sequence 5166, Ap
Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-469-522-34
Sequence 34, Applicant Inc US/09469522
Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Ren, Shi-Xue
Zhou, Yuhui
TITLE OF INVENTION: MODIFIED RETINOLANOMA TUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4434

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Heller, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01XC-506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 3266 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

NAME/KEY: GPS

LOCATION: 7..2502

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US 09 46 452-34

Query Match 100.0%; Score 4266; DB 10; Length 3266;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GGCATCATGCTGCGGAAATGCTATGCTTATTCGACGAGTTCACCTGAGATGAGATGCTCG 60
 QY 61 TTGATTTTATGAGCTGACGATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAA 120
 DB 61 TTGATTTTATGAGCTGACGATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAA 120
 QY 121 GTAAAGAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 180
 DB 121 GTAAAGAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 180
 QY 181 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 240
 DB 181 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 240
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 QY 421 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 480
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 DB 601 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 660
 QY 661 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 720
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 QY 781 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 840
 DB 781 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 840
 QY 841 TATGATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 900
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 QY 1021 GACAGAGTTCGCGGAAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1080
 DB 1021 GACAGAGTTCGCGGAAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1080
 QY 1081 GACAGAGTTCGCGGAAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1140
 DB 1081 GACAGAGTTCGCGGAAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1140
 QY 1141 AACTTTCGATGATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 1200
 DB 1141 AACTTTCGATGATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 1200
 QY 1201 ATGCTTCATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1260
 DB 1201 ATGCTTCATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1260
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 QY 1321 TTTATCAAG 1380
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 QY 1381 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1440
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 QY 1561 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1620
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 QY 1861 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1920
 DB 1861 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1920
 QY 1921 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1980
 DB 1921 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1980
 QY 1981 GATGATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 2040
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1482 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1541
1461 AGTAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 1520
1542 ATTAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 1601
1521 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1580
1602 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1661
1581 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1640
1662 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1721
1641 ATTAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 1700
1722 ATTAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 1781
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1842 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1901
1821 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1880
1902 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1961
1881 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 1940
1962 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2021
1941 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2000
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2001 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2060
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2061 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2120
2142 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2201
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2181 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2240
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2241 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2300
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2382 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2441
2361 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2420
2442 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2501
2421 TGTATGCTGTCAGATACAGCTTATTTGATCTTATTAACAATCAAGCAGCAGAGG 2480
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2481 TACCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2540
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2541 CTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2600
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2601 ACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2660
2682 ACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2741
2661 CATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2720
2742 CATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2801
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2961 AATGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3020
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3102 ATATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 3161
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3261 GATATCT 3266
3342 GATATCT 3347

RESULT 13
US-09-469-522-48
Sequence 48, Application 05/04/95-2
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETIN-BLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET, P.O. Box 4433

1 NAME: Hiblot, David W.
 2 REGISTRATION NUMBER: 41,071
 3 REFERENCE/LOCKER NUMBER: UTXC:506
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: 512/418-3000
 6 TELEFAX: 512/474-7577
 7 INFORMATION FOR SEQ ID NO: 46:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 3477 base pairs
 10 TYPE: nucleic acid
 11 STRANDEDNESS: single
 12 TOPOLOGY: linear
 13 FEATURE:
 14 NAME/KEY: CDS
 15 LOCATION: 7..2613
 16 SEQUENCE DESCRIPTION: SEQ ID NO. 46:
 17 US 09 469 522 46

Query Match 88.4% Score 2886.6 DB 10: length 3377;
 Best local similarity 94.4% Pred. No. 0;
 Matches 4076; Conservative 0; Mismatches 4; Indels 177; Gaps 1;

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 28 298 CTGTGGGCAATCTGATCTTATGTGAGCAGTTGACCTAGATGATGATGCTGCTCAGTTTT 357
 29 76 ATGTAGATACAGAAACATAGAAATCAGTGTGCATATAATCTTTAACTTACTTAAAGAA 129
 30 358 ATGTAGATACAGAAACATAGAAATCAGTGTGCATATAATCTTTAACTTACTTAAAGAA 417
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 44 430 AAATAGATGCTGCTGAT 560
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 49 430 TGTATAAT 729
 50 780 TGTATAAT 840
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 52 840 GAT 900

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 1330 GCAAG 1389
 1440 GCAAG 1500
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 1500 ATGCAATTCCTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1560
 1450 GATGAG 1509
 1560 GATGAG 1620
 1510 AATATCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1569
 1620 AATATCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1680
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 1630 AGCTGAG 1689
 1740 AGCTGAG 1800
 1690 GCTATCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1749
 1800 GCTATCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1860
 1750 CATATCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1809
 1860 CATATCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1920
 1810 AGCTATTCGAG 1869
 1920 AGCTATTCGAG 1980

GenScore version 5.1.3
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M protein nucleic search, using frame_plus_p2n model

Run on: January 18, 2003, 04:41:54 : Search time 62.1223 Seconds
(without alignments)
6107.852 Million cell updates/sec

Files: US-09-026-459A.33

Best score: 4372
Sequence: 1 MEKVSSVGVVIAHYIQRKKE.....TRMKQKMDSDTSNKEEK 851

Scoring Table:

Gapop 10.0 : Gapext 0.5
Gapop 10.0 : Gapext 0.5
Gapop 6.0 : Gapext 7.0
Gapop 6.0 : Gapext 7.0

Searched: 39868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787746

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Command line parameters:

MODEL frame_plus_p2n model -DEV xlib
GAPOP 10.0 GAPEXT 0.5
US-PUBLISHED APPLICATIONS NA -GEMT-FASTAP -SUFFIX-rnpb -MINMATCH-0.1
LOP-LO-0 LOPEXT-0 -UNITS-hits -START-1 -END-1 -MATRIX-blosum62
-TRANS-hmm640 cch 1157-45 -FACALON-200 -THP-SCOPE-pst -THP-MAX-100
-THP-MIN-0 -ALIGN-15 -MODE-LOCAL -CODITMT-PTG -NOM-EXT -HAPSI71-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US04025459-CCON_1_1-509-0-0-0-152139-23369
-N-10-6 -ICPI 3 -NO_XLPHY -LARGE00PHY -NEG_SCORES-0 -WAIT -LONGLOG
DEV TIME/MT-120 -WARN -TIMEOUT-40 -THREAS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
FAPEXT-7 -YGAPOP-10 -YGAPOP-0.5 -DELOP-6 -DELEXT-7

Database: Published Applications NA:

1: /z/qn2/6/ptdata/1/pubna/us07_purc0mb.seq:
2: /z/qn2/6/ptdata/1/pubna/us07_purc0mb.seq:
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5: /z/qn2/6/ptdata/1/pubna/us08_NEW_purc0mb.seq:
6: /z/qn2/6/ptdata/1/pubna/us08_NEW_purc0mb.seq:
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12: /z/qn2/6/ptdata/1/pubna/us10_NEW_purc0mb.seq:
13: /z/qn2/6/ptdata/1/pubna/us10_NEW_purc0mb.seq:
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15: /z/qn2/6/ptdata/1/pubna/us10_NEW_purc0mb.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4372	100.0	3324	10	US-09-469-522-32
2	4367	99.9	3392	10	US-09-469-522-40
3	4367	99.9	3455	10	US-09-469-522-28
4	4367	99.9	4555	10	US-09-469-522-1

RESULT 1

US-09-469-522-32
Sequence 32, Application US/09469522

Patent No. US-6,344,411A1

GENERAL INFORMATION:

APPLICANT: X0, Hong Ji

HO, Shi Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4434

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4434

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.46

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09469522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

Sequence 14, App
Sequence 7, Appl
Sequence 50, Appl
Sequence 34, Appl
Sequence 48, Appl
Sequence 40, Appl
Sequence 6, Appl
Sequence 46, Appl
Sequence 48, Appl
Sequence 46, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 47, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 41, A
Sequence 19910, A
Sequence 296, App
Sequence 406, App
Sequence 336, App
Sequence 216, App
Sequence 163, App
Sequence 292, App
Sequence 115, App
Sequence 186, App
Sequence 2346, App
Sequence 3, Appl
Sequence 1, Appl
Sequence 51, Appl
Sequence 9859, App
Sequence 1242, App
Sequence 145, App
Sequence 3, Appl
Sequence 55, Appl
Sequence 4196, App
Sequence 804, App
Sequence 175, App
Sequence 359, App
Sequence 11, Appl
Sequence 9, Appl

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hlibert, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTIC:506
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2559
 ORIGIN: 469 522-42

Alignment Scores:
 Pred. No.: 0 Length: 3223
 Score: 4372.00 Matches: 851
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-026-459a-33 (1-851) x US-09-469-522-32 (1-3223)

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 Le 7 ALGAGAAAGTTTCATGTGTCATGACATATTGGGAGGTTATATTCAGAAAGAAAGGAA 56
 QY 21 LeuIrpGlyIleCysIlePheIleAlaValAspLeuAspGluMetSerPheThrPhe 40
 Db 67 CTGAGAGAAATGCTATGTTTATTGTAATGTTGATGATGATGATGATGATGATGATGAT 126
 QY 41 ThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLysGlu 60
 Db 127 ACACAGCAGCAGAAACATAGAAACAGAGTCCTCAATAATTCATACATACATACATACAT 186
 QY 61 IleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLysLysLysVal 80
 Le 187 ATTGAATACATAGCAAGGTTGATAATGTTATGTTATGTTATGTTATGTTATGTTATGTT 246
 QY 81 LeuPheAlaIlePheSerLysLeuGluArgThrCysGlnLeuIleTyrLeuThrGlnPro 100
 Db 247 TTGTTTGATCTTCATGTAATGGAAGGACATGTAATGTAATGTAATGTAATGTAATGTAAT 306
 QY 101 SerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerIleThr 120
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 QY 121 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspLeuValIleSerPheGln 140
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 QY 161 ProTyrLysThrAlaValIlePheProIleAsnGlySerProArgThrProArgArgGlyGln 180
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1942 AATCTGGGCTAAATATCACTTGTGAGGCTTCTGCTGAGGACCCAGCAATATAGACAT 2001
622 HistArgGlnIleAsnMetLysSerMetTyrGlyThrCysValLeuAsnIleAsp 641
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662 PheLysArgValLeuIleLysGluGluGluLysAspSerIleLeuValPheTyrAsnSer 681
2122 TCAAAAGGCTTTCATCAACAAAGAGAGAGATGATCTATATAGATCTCTCTCTCTCTCTCT 2181
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2242 TATCAAAATCT 2301
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2662 AGCATGCGATATCTCAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2691
RESULT 4
US-09-469-522-1
Sequence 1, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Ilu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
AFFILIATION NUMBER: US-09-469-522
FILING DATE: 22-Dec-1999
CLASSIFICATION: C01K0605
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC-506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2790
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-469-522-1
Alignment Scores:
Pred. No.: 0 Length: 4555
Score: 4367.00 Matches: 850
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.89% Indels: 0
DB: 10 Gaps: 0
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RESULT 6

US-09-860-211-7
Sequence 7, Application US/09860211
Patent No. US2020147212A1
GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
Wills, Ken N.
Manaval, Daniel C.
TITLE OF INVENTION: Recombinant Adenoviral Vector and Methods of Use
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,211
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,673
FILING DATE: 15-FEB-2000
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-OCT-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-APR 1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 016930-00092005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2925
OTHER INFORMATION: /product= "KH"
/note= "relinblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID No: 7:
US-09-860-211-7
Alignment Scores:

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Score: 4357.00                     Matches: 849
Percent Similarity: 99.888          Conservative: 0
Best Local Similarity: 99.888       Mismatches: 1
Query Match: 99.664                 Indels: 0
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US-09-026-459a 43 (1-851) x US-09-860-211-7 (1-2995)

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1 Bruedict, William F.
 2 Zhou, Yunli
 3 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 4 PROTEINS
 5 NAME OF APPLICANT:
 6 CORRESPONDENCE ADDRESS:
 7 ADDRESS: 20023, White & Barker
 8 STREET, P.O. Box 4433
 9 CITY: Houston
 10 STATE: TX
 11 COUNTRY: USA
 12 ZIP: 77210-4433
 13 COMPUTER READABLE FORM:
 14 MEDIUM TYPE: Floppy disk
 15 OPERATING SYSTEM: IBM PC compatible
 16 SOFTWARE: Patent In Release #1.0, Version #1.30
 17 CURRENT APPLICATION DATA:
 18 APPLICATION NUMBER: US-09-469-523
 19 FILING DATE: 22-Dec-1999
 20 CLASSIFICATION: unknown
 21 PRIOR APPLICATION DATA:
 22 APPLICATION NUMBER: 09/026,459
 23 FILING DATE: unknown
 24 ATTORNEY/AGENT INFORMATION:
 25 NAME: Hibler, David W.
 26 REGISTRATION NUMBER: 41,071
 27 REFERENCE/DOCKET NUMBER: UICX-506
 28 TELEPHONE: 512/418-3000
 29 TELEFAX: 512/474-7577
 30 INFORMATION FOR SEQ ID NO: 40:
 31 SEQUENCE CHARACTERISTICS:
 32 LENGTH: 3461 base pairs
 33 TYPE: nucleic acid
 34 STRANDEDNESS: single
 35 TOPOLOGY: linear
 36 FEATURE:
 37 NAME/KEY: CDS
 38 LOCATION: 7..2697
 39 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
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 42 Alignment Scores:
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 44 Seq. No. Length: 3461
 45 Scores: 4217.00 Matches: 821
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 DB 1804 TATCTGAGCAAT 1863
 QY 602 ThrThrThrPhePheGluHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArg 621
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 : Sequence 48, Application US/09469522
 : Patent No. US29020151461A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Hong-Ji
 : Hu, Shi-Xue
 : Benedict, William F.
 : Zhou, Yunli
 : TITLE OF INVENTION: MODIFIED REINOHLASIOMA TUMOR SUPPRESSOR
 : PROTEINS
 : NIMRP OF SEQUENCE: 51
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Durkee
 : STREET: P.O. Box 4433
 : CITY: Houston
 : STATE: TX
 : COUNTRY: USA
 : ZIP: 77210-4433
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09469,522
 : FILING DATE: 22-Dec-1999
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/026,459
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hibler, David W.
 : REGISTRATION NUMBER: 41,071
 : REFERENCE/DOCKET NUMBER: UICX:506
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 512/418-3000
 : TELEFAX: 512/474-7577
 : INFORMATION FOR SEQ ID NO: 48:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3383 base pairs
 : SYL: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 7..2619
 : SEQUENCE DESCRIPTION: SEQ ID NO: 48:
 US-09-469-522-48
 Alignment Scores:
 Pred. No.: 0 Length: 3383
 Score: 4017.50 Matches: 793


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Job time : 158.122 secs

Genome version 5.1.3
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Run on: January 16, 2003, 15:20:22 : Search time 9.29616 seconds
(without alignments)
16320.741 Million cell updates/sec

Query: US-09-026-459A-32

Partial source: 3425

Sequences: 1 GATCATGAGGAGAAAGTTTC.....AAATGAGGATTAATGATAGT 3323

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searches: 49086 seqs, 22294149 residues 787746

Total number of hits satisfying chosen parameters:

Minimum hit seq length: 0

Maximum hit seq length: 2000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:

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- 2: Z0002_6/pptdata/a1/pptdata/US08_NEW_PUB_seq
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- 4: Z0002_6/pptdata/a1/pptdata/US08_NEW_PUB_seq
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- 11: Z0002_6/pptdata/a1/pptdata/US08_NEW_PUB_seq
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- 13: Z0002_6/pptdata/a1/pptdata/US08_NEW_PUB_seq
- 14: Z0002_6/pptdata/a1/pptdata/US08_NEW_PUB_seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3423	100.0	3423	10	US-09-459-522-32	Sequence 32, Appl
2	3415	99.8	3492	10	US-09-459-522-30	Sequence 30, Appl
3	3415	99.8	3455	10	US-09-459-522-28	Sequence 28, Appl
4	3415	99.8	3555	10	US-09-459-522-1	Sequence 1, Appl
5	3415	99.8	4839	9	US-09-954-531-143	Sequence 143, Appl
6	3311.8	99.7	4554	10	US-09-459-522-50	Sequence 50, Appl
7	327.7	98.0	3256	10	US-09-459-522-34	Sequence 34, Appl
8	3226	97.1	3323	10	US-09-459-522-48	Sequence 38, Appl
9	3225.4	97.1	3461	10	US-09-459-522-40	Sequence 40, Appl
10	3212	96.7	3218	10	US-09-459-522-4	Sequence 4, Appl
11	3107	94.5	3113	10	US-09-459-522-46	Sequence 36, Appl
12	3006	90.5	3347	10	US-09-459-522-42	Sequence 42, Appl
13	2956.6	89.0	3383	10	US-09-459-522-48	Sequence 48, Appl
14	2944.5	88.5	3472	10	US-09-459-522-45	Sequence 46, Appl
15	2827.4	85.1	3161	10	US-09-459-522-44	Sequence 44, Appl
16	2618.4	78.8	2995	10	US-09-860-211-7	Sequence 7, Appl
17	428	12.9	451	9	US-09-796-632-7740	Sequence 7740, Ap
18	142.2	4.3	411	10	US-09-864-761-3141	Sequence 3141, Ap
19	129	3.9	129	10	US-09-864-761-1910	Sequence 1910, A

20	104	3.1	304	10	US-09-964-824A-296	Sequence 296, Ap
21	68.8	2.1	3940	9	US-09-292-758-37	Sequence 37, Appl
22	59.4	1.8	324	9	US-09-796-632-2546	Sequence 2546, Ap
23	51	1.5	3747	10	US-09-770-657-1	Sequence 1, Appl
24	51	1.5	3747	12	US-10-025-676-2	Sequence 2, Appl
25	49.4	1.5	640681	10	US-09-790-988-1	Sequence 1, Appl
26	48.8	1.5	335913	9	US-09-754-853A-2	Sequence 2, Appl
27	48.8	1.5	335913	5	US-09-754-853A-3	Sequence 3, Appl
28	48.4	1.5	419	10	US-09-969-373-442	Sequence 442, Appl
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31	47.8	1.4	424	10	US-09-960-352-11218	Sequence 11218, A
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33	47	1.4	393	10	US-09-960-352-4582	Sequence 4582, Ap
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ALIGNMENTS

RESULT 1

US-09-459-522-32

Sequence 32, Application US-09-459-522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLANOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Fatedit to release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US20020151461A1

FILING DATE: 22-Dec-1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hilbert, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 3423 base pairs

TYPE: nucleic acid

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1991 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2050
1689 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 1748
2051 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2110
1749 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 1808
2111 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2170
1809 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 1868
2171 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2230
1869 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 1928
2231 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2290
1929 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 1988
2291 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2350
1989 TATGAAGATATATATATATTAAGAAATATTTTAAATTTGATTAATTTGATTAATTTG 2048

2351 ATTCAGAAATGATTTTAT 2410
2049 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2108
2411 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2470
2109 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2168
2471 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2530
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2591 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2650
2289 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2348
2651 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2710
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2711 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2770
2409 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2468
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2469 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2528
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2529 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2588
2891 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2950
2589 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2648
2951 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3010
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2709 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2768
3071 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3130
2769 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2828
3131 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3190
2829 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2888
3191 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3250
2889 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 2948
3251 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3010
2949 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3008
3311 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3170
3009 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3068
3371 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3130
3069 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3128
3431 GGTATTCATGACAGACATGAGAAACAAATATATATATATATATATATATATATATATAT 3190

QY 2747 AGTTAGCATGTTATTTATATAAAGATTGAAATCTGTGTAAATCTGCTGCAATTTAAAA 2796
 DB 2527 AATTAGCATGTTATTTATATAAAGATTGAAATCTGTGTAAATCTGCTGCAATTTAAAA 2586
 QY 2747 AGTTAGCATGTTATTTATATAAAGATTGAAATCTGTGTAAATCTGCTGCAATTTAAAA 2856
 DB 2527 AATTAGCATGTTATTTATATAAAGATTGAAATCTGTGTAAATCTGCTGCAATTTAAAA 2586
 QY 2847 AAGGATCTAGAGTGGAGCTGTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2916
 DB 2647 AAGGATCTAGAGTGGAGCTGTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2706
 QY 2917 TAAATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2976
 DB 2707 TAAATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2766
 QY 2977 AATATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3036
 DB 2767 AATATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2826
 QY 3047 GCAATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3096
 DB 2847 GCAATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2946
 QY 3157 GCTGTTTATATAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3216
 DB 2947 GCTGTTTATATAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3006
 QY 3217 GATATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3276
 DB 3007 GATATATAGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3066
 QY 3277 TATTTTATATATAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3323
 DB 3067 TATTTTATATATAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3113

RESULT 12
 US 09 469 522-42
 : Sequence 42, Application US/09469522
 : Patent No. US20020151461A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Boel Ji
 : Bo, Shi-Xue
 : Benedict, William F.
 : Zhou, Yunli
 : TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 : PROTEINS
 : NUMBER OF SEQUENCES: 51
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Durkee
 : STREET: P.O. Box 4433
 : CITY: Houston
 : STATE: TX
 : COUNTRY: USA
 : ZIP: 77210-4433
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US 09/469,522
 : FILING DATE: 22-Dec-1999
 : CLASSIFICATION: <Unknown>
 : PUBLICATION DATA:
 : APPLICATION NUMBER: 09/026,459
 : FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: US 09-506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FILE SEQ ID NO: 42;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3347 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2583
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 59-09-469-522-42

Query Match 96.5%, Score 3066, DB 10; Length 3347;
 Host Local Similarity 100.0%; Prod. No. 0;
 Matches 3066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 AT 377
 DB 342 ATCTACTGAAATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 401
 QY 378 TAAAGGGGAACTATATATAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 437
 DB 402 TAAAGGGGAACTATATATAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 461
 QY 438 TTTCTTGTAT 497
 DB 462 TGTCTTGACAT 521
 QY 436 ATCTTAT 557
 DB 522 ATCTTAT 581
 QY 558 AGGATAGCAAAACAACTAGCAAGATATAGCAAGATATAGCAAGATATAGCAAGATATAG 617
 DB 582 AGGATAGCAAAACAACTAGCAAGATATAGCAAGATATAGCAAGATATAGCAAGATATAG 641
 QY 618 TGAATGTAATATAGATGAGTGAAGAAAGTATATATATATATATATATATATATATAT 677
 DB 642 TGAATGTAATATAGATGAGTGAAGAAAGTATATATATATATATATATATATATATAT 701
 QY 678 TTTCTTGTAT 737
 DB 702 TTTCTTGTAT 761
 QY 738 GCAACAAAT 797
 DB 762 GCAACAAAT 821
 QY 798 AACTCTTCACTGATTTCTATAGACATTTTGAAGAACAGAACACACAGGAAAGAAAGTAA 857
 DB 822 AACTCTTCACTGATTTCTATAGACATTTTGAAGAACAGAACACACAGGAAAGAAAGTAA 881
 QY 858 CTTTGATGAAAGTGAATGATTTATTTCTGCAATATTTCTGCAATATTTCTGCAATATTT 927
 DB 882 CTTTGATGAAAGTGAATGATTTATTTCTGCAATATTTCTGCAATATTTCTGCAATATTT 941
 QY 918 TATCCAAAT 977
 DB 942 TATCCAAAT 1001
 QY 978 TATCCAAAT 1047
 DB 1002 TATCCAAAT 1061
 QY 1038 TATCCAAAT 1097

[illegible]

QY	2178	AGGAAACATCTATATTTCACGGGCTGAAAGAGTCATATAAAATTTTCAGAACTTTGGCAAC	2201
DB	2202	AGGCAACATCTATATTTCACGGGCTGAAAGAGTCATATAAAATTTTCAGAACTTTGGCAAC	2261
QY	2238	ACCANAAAATGACTGAGATCAGAAATCTTAATATTAATGCTGAACTATTGCGAAC	2297
DB	2262	ACCANAAAATGACTGAGATCAGAAATCTTAATATTAATGCTGAACTATTGCGAAC	2321
QY	2298	TTCGCAAACTTCGAGAAAIAAAACATAGGATATCAACATCAACGCTGCTCAAAAC	2357
DB	2422	TTCTGAGAACTTCGAGAAAIAAAACATAGGATATCAACATCAACGCTGCTCAAAAC	2481
QY	2458	AAAGAGGAGAAAGCAAGGCTCTAAACATGAGAAAAATAGCTTTGATATGAAG	2417
DB	2482	AAAGAGGAGAAAGCAAGGCTCTAAACATGAGAAAAATAGCTTTGATATGAAG	2441
QY	2418	ATCAGATGAACAGATGAAGTAAAATATGAGGAGCAATGCTGAAATTTACAAAACT	2477
DB	2442	ATCAGATGAACAGATGAAGTAAAATATGAGGAGCAATGCTGAAATTTACAAAACT	2501
QY	2478	GGCAGAAATGACTTCTGACACAGAAATGAAAGGAGAAAAAGAAATAGATAGGAA	2537
DB	2502	GGCAGAAATGACTTCTGACACAGAAATGAAAGGAGAAAAAGAAATAGATAGGAA	2561
QY	2538	TAGCTCAAAAGAGGAGAAATGAGGATCTAGGAGCTTGGGAGCAATGCTCAAACT	2597
DB	2562	TAGCTCAAAAGAGGAGAAATGAGGATCTAGGAGCTTGGGAGCAATGCTCAAACT	2621
QY	2598	CTGGATTCATGTCTCTCAACAGATGAGATGAATCTTGGAGGCTGCTTAAGGCG	2657
DB	2622	CTGGATTCATGTCTCTCAACAGATGAGATGAATCTTGGAGGCTGCTTAAGGCG	2681
QY	2658	ACATTTAAATATCTTCAGCTCTCTTCGAGAAIAAAAATGCGACAAATGCTTCGAGT	2717
DB	2682	ACATTTAAATATCTTCAGCTCTCTTCGAGAAIAAAAATGCGACAAATGCTTCGAGT	2741
QY	2718	GATTCCTAAAGCACTTGAATTTAGCTATTCTTATTATATCAATGTCGAAATCTTGTG	2777
DB	2742	GATTCCTAAAGCACTTGAATTTAGCTATTCTTATTATATCAATGTCGAAATCTTGTG	2801
QY	2778	TAAATCTGCAATTTAAAAAGTTGTACACATGTTGCTCTCTCAAACTAAATTTGCTG	2837
DB	2802	TAAATCTGCAATTTAAAAAGTTGTACACATGTTGCTCTCTCAAACTAAATTTGCTG	2861
QY	2838	TGCTTTTAGCATAGAAAGAAAGGCTACAGTGGAGGCTGATCAACGAGCTGCTG	2897
DB	2862	TGCTTTTAGCATAGAAAGGCTACAGTGGAGGCTGATCAACGAGCTGCTG	2921
QY	2898	ACTAATTTGCTCTCTCTTGGAGATATAGTAAGTTGCTCTCTCTTTTATTAATTTAT	2957
DB	2922	ACTAATTTGCTCTCTCTTGGAGATATAGTAAGTTGCTCTCTCTTTTATTAATTTAT	2981
QY	2958	ATGATATTTTTTTTAAATTAACATGAACACGCTTACAAAATGCTGCTATATCTTCCA	3017
DB	2982	ATGATATTTTTTTTAAATTAACATGAACACGCTTACAAAATGCTGCTATATCTTCCA	3041
QY	3018	AATGCAATTTGATGATGCTGCCCAATGCAACAAAATTAAGTCTGCTGCGAAAAAGG	3077
DB	3042	AATGCAATTTGATGATGCTGCCCAATGCAACAAAATTAAGTCTGCTGCGAAAAAGG	3101
QY	3078	ATATTATTCAAAATTAACAAAATTTACTAAATTTTCAATATGATTTTTTATTATTAT	3137
DB	3102	ATATTATTCAAAATTAACAAAATTTACTAAATTTTCAATATGATTTTTTATTATTAT	3161
QY	3138	GGAATCTGATATAGCTGTGCTGTTTATAAAATTTGCTTTAAATTAATAAATAAGCTG	3197
DB	3162	GGAATCTGATATAGCTGTGCTGTTTATAAAATTTGCTTTAAATTAATAAATAAGCTG	3221
QY	3198	GAGCAAGATTAACCAATAGATATCAATCAATCACTCAAAACAGATTAATCACTTCAAA	3257
DB	3222	GAGCAAGATTAACCAATAGATATCAATCAATCACTCAAAACAGATTAATCACTTCAAA	3281

GENERAL INFORMATION:

APPLICANT: Xu, Hong-di
Hu, Shi-xue
Boudict, William F.
Zhao, Yunli

TITLE OF INVENTION: MODIFIED RETINORASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: 22 Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: DTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 3377 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME: KEY: CTS

LOCATION: 7..2614

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US 09 469 522-46

Query Match 88.6% Score 2944.6; DB 10; Length 3377;

Best Local Similarity 94.5%, Freq. No. 6.

Matches 4134; Conservative 0; Mismatches 4; Indels 177; Gaps 1;

QY 4 GGACAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGGAAGT 68
DB 240 GGACAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGGAAGT 299
QY 69 GTGAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGGAAGT 128
DB 300 GTGAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGGAAGT 359
QY 120 TGAATTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 188
DB 480 TGAATTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 419
QY 184 TGAATTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 248
DB 420 TGAATTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 479
QY 249 GTTTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 308
DB 480 GTTTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 539
QY 400 TGAATTCACAAAGAAAGTTCATCTGGGAGGAGATGGGAGGTATATATTCACAAAGAAAGT 368
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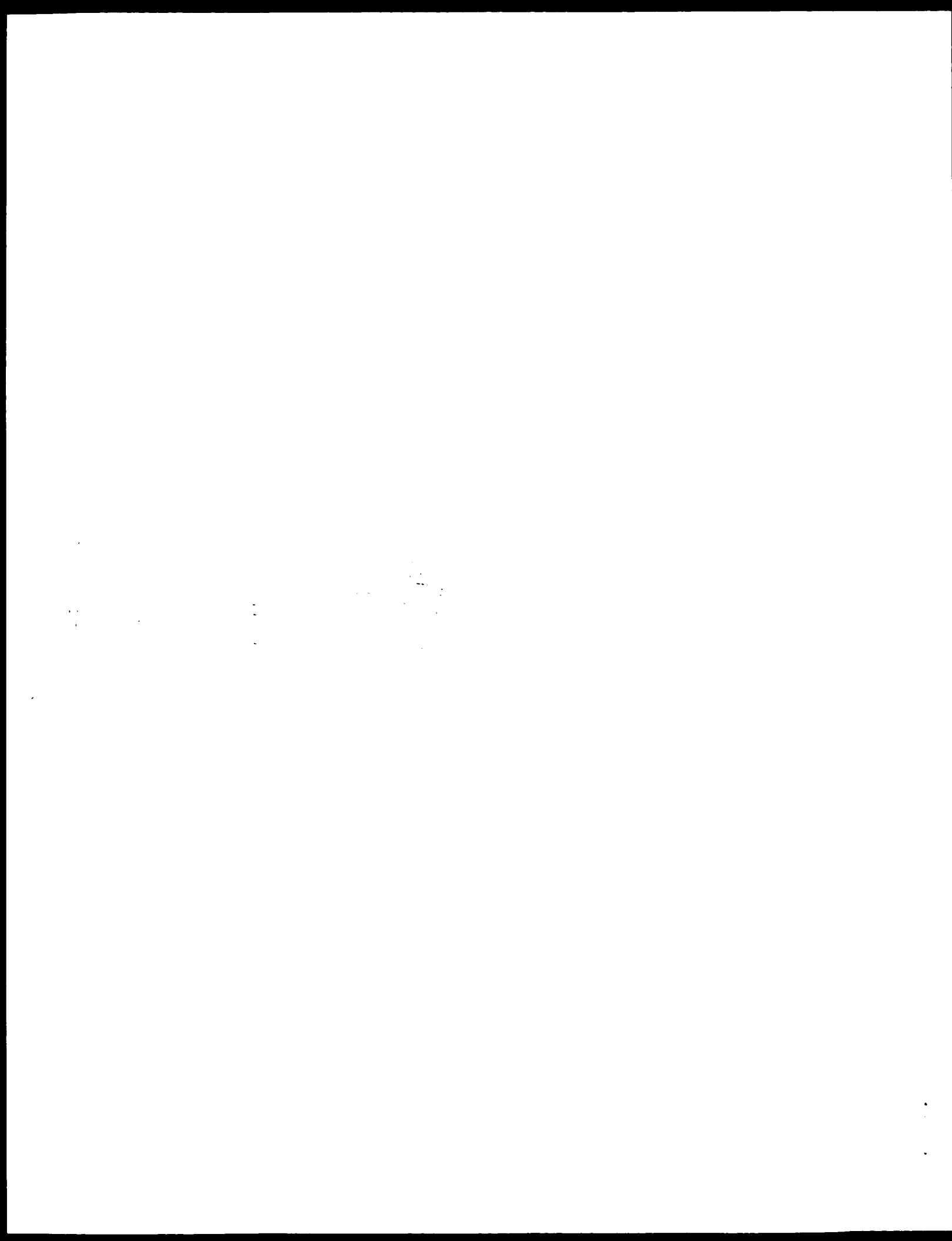
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QY 429 AATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
DB 549 ----- 548
QY 489 ATATATAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB 549 ----- 548
QY 549 CAGGAGTTCAGGATAGCAAAACATAGAAATGATAGAAATATTATTCAGTTCCTGCTG 608
DB 608 CAGGAGTTCAGGATAGCAAAACATAGAAATGATAGAAATATTATTCAGTTCCTGCTG 662
QY 609 TAAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
DB 668 TAAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 722
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DB 728 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 782
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DB 788 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 842
QY 842 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 848
DB 848 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 902
QY 902 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 908
DB 908 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 962
QY 962 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 968
DB 968 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1022
QY 1022 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1028
DB 1028 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1082
QY 1082 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1088
DB 1088 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1142
QY 1142 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1148
DB 1148 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1202
QY 1202 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1208
DB 1208 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1262
QY 1262 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1268
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QY 1322 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1328
DB 1328 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1382
QY 1382 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1388
DB 1388 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1442
QY 1442 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1448
DB 1448 TTTATTCGTAAGAGGCAAGCTATTACAAATGAGAGATGATCTGTGATTCATTCACT 1502

COUNTRY: USA
 ZIP: 77210 4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FastIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 44:
 LENGTH: 3161 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2497
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Query Match 85.1%; Score 2827.4; DB 10; Length 3161;
 Best Local Similarity 99.6%; Prod. No. 0;
 Matches 2834; Conservative 0; Mismatches 11; Indels 0; Gaps 0.

1019 TACTGAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGAG 1078
 857 TACUGAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGAG 916
 1079 GACAGGCTTGTGTGAAATTTGGATACAGAGATACAACTTGGAGTTGGCTTGTATATAG 1138
 617 GATAGGCTTGTGTGAAATTTGGATACAGAGATACAACTTGGAGTTGGCTTGTATATAG 976
 1139 GATAGGCTTGTGTGAAATTTGGATACAGAGATACAACTTGGAGTTGGCTTGTATATAG 1198
 977 GATAGGCTTGTGTGAAATTTGGATACAGAGATACAACTTGGAGTTGGCTTGTATATAG 1036
 1199 AATTTTGAAT 1258
 1037 AATTTTGAAT 1096
 1259 TGGCATAATATAGGAT 1318
 1097 TGGCATAATATAGGAT 1156
 1319 CATGATTTGCAATTTGCTTAAATTTAAAGGCTTTGATTTTACAAGGATGATGAAAGT 1378
 1157 CATGATTTGCAATTTGCTTAAATTTAAAGGCTTTGATTTTACAAGGATGATGAAAGT 1216
 1379 TTATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1438
 1217 TTATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1276
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 1277 ATCCAAATCATGGAATGCTTGGATGATGATGATGATGATGATGATGATGATGATGATG 1336
 1499 AATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1558
 1337 AATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1396
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 1397 CTTCTGAAAT 1456
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 1919 AATTAGAAT 1978
 1757 AATTAGAAT 1816
 1979 TCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2038
 1817 TCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1876
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 1877 TCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1936
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479 TCAGAGAGGAT 538
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 719 AATGAGAGGAT 778
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 959 AATGAGAGGAT 1018
 797 AATGAGAGGAT 856



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OM protein: nucleic search using frame_plus.pgm model

Run on: January 18, 2003, 04:31:54 : Search time 6x 8013 seconds
(without alignments)
6107.852 Million cell updates/sec

File: us-09-026-459a-31

Perfect score: 4504

Sequence: 1 MDTALCQKTKIFHVRFA.....TMMQKKNUSMTSNREK 874

Scoring table:

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Searched: 93868 seqs, 2294149 residues

Total number of hits satisfying chosen parameters: 787746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 4% summaries

Command line parameters:

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-THP-MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pyo -NORM-ext -HEAPSIZE-500 -MINLEN-0
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Database:

Database	Published Applications NA
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4499	99.9	4495	10	US-09-469-522-28
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4	4499	99.9	4869	9	US-09-954-531-143
					Sequence 30, Appl
					Sequence 28, Appl
					Sequence 1, Appl
					Sequence 143, Appl

5	4489	99.7	2995	10	US-09-860-211-7	Sequence 7, Appl
6	4489	99.7	3554	10	US-09-469-522-50	Sequence 50, Appl
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8	4307	95.6	3461	10	US-09-469-522-40	Sequence 40, Appl
9	4273	94.9	3266	10	US-09-469-522-34	Sequence 34, Appl
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45	125.5	2.8	4780	10	US-09-962-436-287	Sequence 287, Ap

ALIGNMENTS

RESULT 1

us-09-469-522-30
Sequence 30, Application US/09469522
Patent No. US20020151461A1

GENERAL INFORMATION

APPLICANT: Xu, Hong Ji
Hu, Shi-Xiao
Benedit, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLAST-MA TOM-B SUPPRESSOR

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Burke
CITY: Houston
STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-Dec 1999

CLASSIFICATION: <Unknown>


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US 09 469 522 28
Sequence 28, Application US/99469522
Patent No. US2002015146A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Hendrick, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS

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NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99469522
FILING DATE: 22 Dec 1999
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Hiblot, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTX: 506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 3455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2491
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-026-459-522-28
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Score: 4499.00 Matches: 874
Percent Similarity: 100.00% Conservations: 0
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DB 2272 TATAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2331
QY 722 ThrGluThrLeuSerProThrPheHisIlePheArgSerProTyrLysPheProSer 741
DB 2332 GAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2391
QY 742 ProLeuArgIlePheThrGluAsnIlePheLeuSerProLeuLysSerProThrLysGlu 761
DB 2392 GAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2451
QY 762 SerGluGluLeuProThrProThrLysMetThrPheArgAspArgIleLeuValSerIle 781

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DB 2452 TCAGAGGCTTCGCAATTCACACCAAAATGACACCAATTCACCAATTCACCAAT 2511
QY 782 GlyGluSerPheGlyThrSerGluLysPheGluLysIleAsnGlnMetValCysAspSer 801
DB 2512 GATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2571
QY 802 AspArgValIleLysValSerAlaGluGluLysSerAspPheProLysPheLeuLysSer 821
DB 2572 GACGCGTGGCTCAAAACAAAGTCTGAGGAGCAACACCTCTAAACCACTGCAAAAC 2631
QY 822 ArgPheAspIleGlyThrSerAspGluAlaAspGlySerLysHisLeuProGlyValSer 841
DB 2632 GATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2691
QY 842 LysPheGluGluLysIleValGluMetThrSerThrArgIleThrArgGluGluLys 861
DB 2692 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2751
QY 862 MetAspAspSerMetAspThrSerAsnLysGluGluLys 874
DB 2752 ATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2799

```

RESULT 4

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US-09-954-531-143
; Sequence 143, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Wadsworth
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/56/234,509
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-143

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Alignment Scores:
Pred. No.: 0 Length: 4839
Score: 4499.00 Matches: 873
Percent Similarity: 100.00% Gaps: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0

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US-09-026-459a-31 (1-874) x US-09-954-531-143 (1-4839)

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QY 2 AspPheThrAlaIleCysGlnLysIleCysValIleArgValArgValArgVal 21
DB 363 GATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 362
QY 22 LeuThrIleGluLysValSerValAspGlyValLeuGlyLysIleTyrIleGluLysLys 41
DB 363 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 422
QY 12 LysGluGluThrPheGluLysIlePheLeuAlaValAspIleAspGluMetSerPhe 61
DB 423 AAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 482

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1912 TTGAGAGACAAAGCATGAAATCACTGCTTTCACTGTTTATAAAAAAGTGAT 1971
602 ATGAGAGAGTLeuValLeuAspThrLeuGlySerGluLeuSerGluHisProGlu 621
1972 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGACAGAGAA 2031
622 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAGAG 641
2032 TTAGAAAT 2091
642 ATGAGAGAGTLeuValLeuAspThrLeuGlySerGluLeuSerGluHisProGlu 661
2092 AGAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2151
662 AGAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 681
2152 AATATAGAGTAAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2211
682 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 701
2212 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2271
702 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 721
2272 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2331
722 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 741
2332 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2391
742 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 761
2392 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2451
762 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 781
2452 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2511
782 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 801
2512 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2571
802 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 821
2572 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2631
822 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 841
2632 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2691
842 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 861
2692 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2751
862 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 881
2752 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 2811

RESULT 7

US 09 469 522 42
Sequence 32, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4434
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469522
FILING DATE: 22-Dec-1999
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: DXC-506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3424 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2559
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-469-522-32

Alignment Scores:
Pred. No.: 0 Length: 3424
Score: 4367.00 Matches: 850
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 96.96% Indels: 0
DB: 10 Gaps: 0

US-09-026-459A-31 (1-874) x US-09-469-522-32 (1-3423)

QY 25 CAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 44
DB 10 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 69
QY 45 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 64
DB 70 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 129
QY 65 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 84
DB 130 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 189
QY 85 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 104
DB 190 GAGGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 249
QY 105 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 124
DB 250 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 309
QY 125 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 144
DB 310 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 369
QY 145 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 164
DB 370 TTAGAGAGTATCTGGGTAAATACATTTGGGAAAGGCTGGTGGAGAGAGAG 429

QY 442 AlaThrTyrSerArgSerThrSerglnAsnLeuAspSertglyThrAspLeuSerPhePro 461
 DB 1499 GGCACATATACGACAGACATCATCAAACTCTTGATCTCGAAGACAGATCTGCTCCCA 1458
 QY 462 TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPhe 481
 DB 1455 TGGATCTGGAATGCTTAATTTTAAAGGCTTTGATTTTACAAAGTGATCGAAGATTTT 1518
 QY 482 CileysAlaGluGlyAsnSerThrArgGluMetIleCysHisGluCysGluHis 501
 DB 1519 ATCAAAATAGAAAGGAAATTGAAAGAGAAATGATAAATCAITTAGAGGATGTAACAT 1578
 QY 502 ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGln 521
 DB 1579 GCAATCAAGCAATCCCTCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAG 1638
 QY 522 SerTyrAspArgGluGlyIleProThrAspHisLeuGluSerAlaTyrProLeuAsnLeuPro 541
 DB 1639 TCAAGGACCGAAAGAGAAATGATTAATCAATTTGAAATCTGATGCTGATTAATTTT 1598
 QY 542 LeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561
 DB 1699 CTCAGAAATATACACATGACATGACATGATATGATCTTCTCTGTAGATCTCCCAAGAAA 1758
 QY 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
 DB 1759 AAAGCTTCTCAATAGCGCTGCTAAATCTCTGCAATGCAAGATCCAGACACACCACTCAGCC 1818
 QY 582 PheGlnThrGlnLysPheLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr 601
 DB 1819 TTTCAGACCGCAAGACCAATGAAATCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1878
 QY 602 ArgLeuAlaTyrIleuArgLeuAsnThrIleuCysGluArgIleuLeuSerGluHisProGlu 621
 DB 1879 GAGTAGCTATCTCGGATTAATATAATTTGTSAAAGCTTTGTTGAGCAAGAGAAA 1938
 QY 622 LeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGlnLeuMet 641
 DB 1939 TTAGAACATAICATCTGACCT 1998
 QY 642 ArgAspAlaIleIleLeuAspSerIleLeuMetMetCysAspMetTyrGlyLeuValLys 661
 DB 1999 AGAAGCAAGATTTGAGAAATATATATATATATATATATATATATATATATATATAT 2058
 QY 662 AsnIleAspGluLysPheLysIleIleValThrAlaTyrIleAspLeuTrpHisAlaVal 681
 DB 2059 AATATAGAGCTTAAATCAAAATCAATTTGTAATATATATATATATATATATATATAT 2118
 QY 682 GluGluThrPheCysArgValLeuIleLysGluGluGlyTyrAspSerIleIleValPhe 701
 DB 2119 CAGACATATATCAAAAGCTTTTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2178
 QY 702 TyrAsnSerValPheMetGlnArgIleLysThrAsnIleLeuGlnTyrAlaSerThrArg 721
 DB 2179 TATAACTGCT 2238
 QY 722 ProThrThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSer 741
 DB 2239 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2298
 QY 742 ProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIle 761
 DB 2299 ACCCTTACGCAATCCGAGAGSACATCTATTTTCCCTCCCTCCCTCCCTCCCTCCCTCC 2358
 QY 762 SerGlnIleLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
 DB 2359 TCAAAAGCTGCTGCAATCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2418
 QY 782 GlyLeuSerIleCysArgSerThrGlnGluGluGluGluGluGluGluGluGluGlu 801
 DB 2419 GGTAAATCTCGGATTTCTGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2478

QY 802 AspArgValIleuLysArgSerAlaGluGlySerAspProProLysProLysLysLeu 821
 DB 2479 CACCTGCTGCTCAAAACACAGCTGCTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2538
 QY 822 ArgPheAspIleCysGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 841
 DB 2539 CAGTCTTATATTCAATCATATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2598
 QY 842 LysPheCysGlnLysLeuAlaGluMetThrSerIleAlaIleArgMetCysLysGluLys 861
 DB 2599 AATTTTCAGCAGAAATCCGAGAAATGACCTCTACTCCAGCAGAAATCCGAGAAATCC 2658
 QY 862 MetAsnAspSerMetAspThrSerAsnLysGluGluLys 874
 DB 2659 ATCAATCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2697

RESULT 9

US-09-469-522-34

: Sequence 34, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Burkee

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

: COUNTRY: USA

: ZIP: 77210-4433

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US-09-469,522

: FILING DATE: 22-Dec-1999

: CLASSIFICATION: G06K9/00

: PRIORITY APPLICATION DATA:

: APPLICATION NUMBER: US-09-469,459

: FILING DATE: <Unknown>

: ATTORNEY/AGENT INFORMATION:

: NAME: Hibler, David W.

: REGISTRATION NUMBER: 41,071

: REFERENCE/DOCKET NUMBER: UTIC:506

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 512/418-3000

: TELEFAX: 512/474-7577

: INFORMATION FOR SEQ ID NO: 34:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3266 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: Single

: TOPOLOGY: linear

: FEATURE:

: NAME/KEY: CDS

: LOCATION: 7..2502

: SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-09-469-522-34

Alignment Scores:

Pred. No.:	0	Length:	3266
Score:	4273.00	Matches:	831
Percent Similarity:	100.00%	Substitutions:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.87%	Indels:	0
DB:	10	Gaps:	0

US 09 026 459A 41 (1-874) x 20 09 469-522 44 (1 3266)
 44 LeuThrPheGlyLeuGlySerPheGluAlaValAspLeuAspGluMetSerPheThrPhe 63
 10 CAGCGGAGAAATCGATATTTATGACAGCAATGACATGATGATGATGATGATGATGAT 69
 64 ThrGluLeuGlnLysAsnGluLeuLeuSerValHisLysPhePheAsnLeuLeuLysGlu 83
 70 AAGAGCTACACAAAAAACAACAAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
 84 HisAspThrSerThrLysValAspAsnGluAlaValAspLeuLeuGlySerThrAspVal 103
 140 ATGGATACAGATGACAAAG 149
 104 LeuPheAlaLeuPheSerLysLeuGluAlaThrCysGluLeuLeuLeuLeuGlnPro 123
 160 TTGTTGACAGCTTGACGCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 249
 124 SerSerSerHisSerThrGluHisAsnSerAlaLeuValLeuLysValSerTrpIleThr 143
 250 AATAGTGCATATGATGAG 309
 144 PheLeuLeuAlaLysGluValLeuGluMetGluAspAspLeuValHisSerPheGlu 163
 310 TTTTATTAGGAG 369
 164 LeuMetLeuCysValLeuAspTrpIleLeuLysLeuSerProProMetLeuLeuLysGlu 183
 370 TTAATGCTATGCTGCTGCTATTTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 184 ProTrpLysThrAlaValIleProLeuAsnGlySerProArgThrProArgArgGlyGlu 203
 430 GCAATAAACAGCTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489
 204 AsnArgSerAlaArgIleAlaLysGluLeuGluAspThrArgIleIleGluValLeu 223
 490 AACAGAGTGCAGGATAG 549
 224 CysGlySerHisSerLysAsnGluAspGluValHisAsnValTrpPheCysAsnPheIle 243
 550 TGTAAAG 609
 244 ProPheMetAsnSerLeuGluLeuValThrSerAsnGlyLeuProGluValGluAsnLeu 263
 610 GTTTTAAAG 669
 264 SerLysArgTrpGluGluIleTrpLeuLysAsnLysAspLeuAspAlaArgLeuPheLeu 283
 670 TTAAG 729
 284 AspHisAspLysThrLeuGluHisAspSerIleAspSerPheGluThrGluArgThrPro 303
 730 GATCATGATTAATTCCTCAGAGCTGATCTATAGAGAGAGAGAGAGAGAGAGAGAGAG 789
 304 ArgLysSerAsnLeuAspGluValAsnValIleProProHisThrProValArgThr 323
 790 GAAAAAG 849
 324 ValMetAsnThrIleGluGluLeuMetMetIleLeuAsnSerAlaSerAspGluProSer 343
 850 GTTATGAG 909
 344 GluAsnGluIleSerTrpPheAsnGlySerValValAsnProLysGluSerIleLeuLys 363
 910 GAAAAATCATTTGATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969
 364 ArgValLysAspIleGlyTrpIlePheLysGluLysPheAlaLysAlaValGlyGlyGly 383
 970 AATGAG 1029
 384 CysValGluIleGlySerGluArgTrpLysLeuGlyValArgLeuTrpTrpArgValMet 403

DB 1030 TGTGTGCAAAATGGATGACAGGATACAAAATTGAGATTGCTGTATTATTCAGAAATG 1089
 QY 404 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGluAsnPheSerLysLeuLeu 424
 DB 1090 GAATCCATGCTTAAATACAAACAGCAACGATTAACCAATGAAAAATTTTACAAATGTC 1149
 QY 424 AsnAspAsnIlePheHisMetSerLeuLeuAlaLysAlaLeuGluValValMetAlaThr 443
 DB 1150 AATGCAACATTTTTCATATCTCTTATATGCGGCGGCTTTCAGAGTTCATAAGAGACA 1209
 QY 444 TrpSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProTrpIle 463
 DB 1210 TATACAGAAATACATCTCAGAAATCTGATCTGAAATGAAATTTGTTTCTTCTGATGAT 1269
 QY 464 LeuAsnValLeuAsnLeuLysAlaPheAspPheTrpLysValIleLeuSerPheIleLys 483
 DB 1270 CTGAATGCTTAAATTAAGAGCTTTCATTTTACAAAGAGAGAGAGAGAGAGAGAG 1429
 QY 484 AlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluAlaLysGluHisArgIle 503
 DB 1330 GCAGAACGCAACCTTCATAGAGAAATGCAAAATATTTAGAAATGAGGAAATGAAAT 1389
 QY 504 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysHisSerLys 524
 DB 1390 ATGGATGCTTGAATGCTGAGATTCATGATTCATTTTATGATCTTATTAAGAAATGAA 1449
 QY 524 AspArgGluGlyProIleAspHisLeuGluSerAlaLysProLeuAsnLeuProLeuGln 543
 DB 1450 GACCCAG 1509
 QY 544 AsnAsnHisThrAlaAlaAspMetTrpLeuSerProValArgSerProLysLysLysGly 563
 DB 1510 AATAATCAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
 QY 564 SerThrArgValAsnSerThrAlaAspAlaGluThrGluAlaThrSerAlaPheGln 583
 DB 1570 TCAGCTAG 1629
 QY 584 ThrGlnLysProLeuLysSerThrSerLysLeuPheTrpLysLysValTrpArgGln 603
 DB 1630 ACCCAAG 1689
 QY 604 AlaTrpLeuArgLeuAspThrLeuCysGluArgLeuLeuSerGluHisProGluGlu 623
 DB 1690 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1749
 QY 624 HisIleIleTrpIlePhePheGluHisThrLeuGlnAsnGluTrpGluLeuMetArgAsp 643
 DB 1750 CATATCATCTGAG 1809
 QY 644 ArgHisLeuAspGlnIleMetMetCysSerMetTrpGlyIleCysLysValLysAsnIle 663
 DB 1810 AGGCATTTGGAGCAAAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1869
 QY 664 AspLeuLysPheLysIleValThrAlaTrpLysAspLeuProHisAlaValGluGln 683
 DB 1870 GACCTTAAATTCACAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1929
 QY 684 ThrPheCysArgValLeuLeuLysGluGluGluTrpAspSerIleIleValPheTrpAsn 703
 DB 1930 ACATTCAAAGCTGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1989
 QY 704 SerValPheMetGluArgLeuLysThrAsnIleLeuGlnIleValAlaSerThrArgProPro 723
 DB 1990 TGGGTCTTCATCCAG 2049
 QY 724 ThrLeuSerProIleProHisIleProArgSerProTrpLysPheProSerProLeu 743
 DB 2050 ACTTGTGACCAATACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2109
 QY 744 ArgIleProGlyGlyAsnIleIleSerProLeuLysSerProTrpLysIleSerGlu 763
 DB 2110 GGGATCTTGGAG 2169

QY 764 GlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGlu 783
 DB 2170 GATCTGACACACACAAACAAATGACATCCAGATCATATATATCTCTCA 2229
 QY 784 SerPheGlyThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 803
 DB 2230 TCAATGCGACATGACAAATGACAAATGACAAATGACAAATGACAAATGACAAAT 2289
 QY 804 ValLeuLysAspSerAlaGlyLysSerAsnProProLysProLysLysLysLeuArgPhe 823
 DB 2290 GAGCAGAAACGAGATGACAGAAACGAGATGACAGAAACGAGATGACAGAAAC 2349
 QY 824 AsnIleGlnGlySerAspGlnLysAspCysLysSerLysHisLeuProGlyLysSerLysPhe 843
 DB 2450 GATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2409
 QY 844 GlnGlnLysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsn 863
 DB 2470 CAGCAGAAACGAGCAGAAACGAGCAGAAACGAGCAGAAACGAGCAGAAACGAG 2469
 QY 864 AsnSerMetAspThrSerAsnLysGlnLysLys 874
 DB 2470 GATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2502

RESULTS

US 09 469 522 38

Sequence 38, Application 09/09469522

Patent No. US 20030151461A1

GENERAL INFORMATION

APPLICANT: Xu, Hui-qin

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/026,459,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Bidler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-1000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2559

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-026-459a-31 (1-874) x US-09-469-522-38 (1-323)

Alignment Scores:

Prod. No.: 0 Length: 323

Score: 4217.00 Matches: 821

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 93.63% Indels: 0

DB: 10 Gaps: 0

US-09-026-459a-31 (1-874) x US-09-469-522-38 (1-323)

QY 54 ValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGluLeuSer 73
 DB 97 GTGACCTTAATACAGATGCTGTTCACTTTTATGAGCTACAGAGAGAGAGAGAGAGAG 156
 QY 74 ValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 93
 DB 157 GTCCATAAATCTTTAACTTACTTAAAGAGAAATTCATACAGTACGCAAGTTCATAAAG 216
 QY 94 MetSerArgLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 113
 DB 217 ATGTCACACACTGTGTGAG 276
 QY 114 ThrCysGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 133
 DB 277 ACATGTGACCTTATATATTTGACACAAACGAGCAGTTCGATATCTACTGAAATAAATTC 336
 QY 134 AlaLeuValLeuLysValSerTrpIleTrpTrpLeuLeuLeuLeuLeuLeuLeuLeuLeu 153
 DB 337 GATGTGCTTAAAGTTCCTGCAATCAATTTTATTAGCTAAAGGGGAGAGATATACAA 396
 QY 154 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 173
 DB 397 ATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456
 QY 174 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleTrpIleAsn 193
 DB 457 AAATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 516
 QY 194 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysLysLeu 213
 DB 517 GCTTCATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 576
 QY 214 GluAsnAspThrArgIleIleGluValLeuGlyLysGluIleGluCysAsnIleAspGln 233
 DB 577 GAAATGATACAGAGATTTATTAAGTTCCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAG 636
 QY 234 ValLysAsnValLysPheCysAsnPheIleTrpPheMetAspSerLeuGlyLeuValThr 253
 DB 637 GTTAAATCTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 696
 QY 254 SerAsnGlyLeuProGluValGlnAsnLeuSerLysArgTyrGlnGlnIleTyrLeuLys 273
 DB 697 TCTAAATGAGCTTCCACAGGTTGAAATCTTCTTAAACGATACGAGAGAAATTTATCTTAA 756
 QY 274 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 293
 DB 757 AATAAGATCATAGATCAGAGATTTATTTGGATCATGATAAACCTCTTCAGATCTGATCT 816
 QY 294 IleAspSerPheGlnThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 313
 DB 817 ATACATCTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 876
 QY 314 ValIleProIleThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 433
 DB 877 GTAAATCTTCCACACATCCAGTACGACCTGTATTCAGACACTATCCCAATTTAAATGAT 936
 QY 334 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerLysPheAsnAspLys 453
 DB 937 ATTTTAAATTCAGTAACTGATTAATCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
 QY 354 ThrValAspProLysGluSerIleLeuLysArgValLysAspIleCysTyrIleLeuLys 173

SEQUENCE CHARACTERISTICS:

LENGTH: 3218 base pairs

TYPE: nucleic acid

STRAND/DN/SS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2454

SEQUENCE DESCRIPTION: SEQ ID NO. 3.

US-09-469-522-3

Alignment Scores:

Fred. No.: 0
 Score: 4192.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 93.07%
 Indels: 0
 Gaps: 10

US-09-469-522-3 (1-874) x US-09-469-522-3 (1-3218)

QY MetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePhe 78
 DB AIGTGTTGCACTTTTCTGAGCTACAGAGAAAACATAGAAATCATGCTGCTAATAATCTTT 66
 QY AsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeu 98
 DB AACCTAACAAAAAATGATACCAAGTACCAAACTTCATATCTATGTCACACACGTGTC 126
 QY LysLysTyrAspValLeuPheAlaLeuPheSerLysLysGluArgThrCysGluLeuIle 118
 DB AAGAAGTAAGTAAGTAATGTTGCACTCTTCAGCAAAATGGAAAGGACATGTGAACCTATA 186
 QY TyrLeuThrGlnProSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLys 138
 DB TATTGACACACCAACCAATTCATATCTACTCAATAAATTTCTGATTCGTGTAAA 246
 QY ValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspLeu 158
 DB GTTCTTTGGAICACATTTTATTACCTTAAAGGGGCAAGTATTACAAATGCAAGATGCTG 306
 QY ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProPro 178
 DB GTGATTTGATTTGAGTAAGTGTGCTGCTGACATTTTATTAAATCTCACTGCTCC 366
 QY MetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 198
 DB AAGTGTGCAACCAACCAATTAATAAATGATTAATGATTAATGATTAATGATTAATGAT 426
 QY ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArg 218
 DB AAGTGTGCAACCAACCAATTAATAAATGATTAATGATTAATGATTAATGATTAATGAT 486
 QY IleIleGluValLeuCysLysGluIleGluCysAsnIleAspGluValLysAsnValTyr 238
 DB ATATTGAACTTCTCTTAAGAACATCATGATTAATATAGATGAGTGAATAATGTTTAT 546
 QY PheLysAsnPheIleProPheMetAsnSerLysGlyLeuValThrSerAsnGlyLeuPro 258
 DB TTTCAAAAATTTTATACCTTTTATTAATCTCTGGAATTTGATTAATGATTAATGATTAAT 606
 QY GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAspLeuAsp 278
 DB GAGGTTGAAAATCTTTCAACGATACCAAGAAATTTATCTTAAAAATTAAGATCTAGAT 666
 QY AlaArgLeuPheLeuAspLysAspLysThrLeuGlnThrAspSerIleAspSerPheGlu 298
 DB GCAAGATTTTGTGAT 746
 QY ThrGlnArgThrProArgLysSerAsnLeuAspGluGluValIleProProHis 318
 DB AAGTGTGCAACCAACCAATTAATAAATGATTAATGATTAATGATTAATGATTAATGAT 786

QY ThrProValArgThrValMetAsnThrIleGlnIleLeuMetIleLeuAsnSerAla 338
 DB ACTCCAGTTAGGACTGTTATCAACACATACCAACAAATTAATGATGATTTTAAAAICACGA 846
 QY SerAspGlnProSerGluAsnIleSerTyrPheAsnAsnCysThrValAsnProLys 358
 DB ASGATATCAAAATTTTCAAAATTTATTTTAAATTAATTAATTAATTAATTAATTAAT 906
 QY GluSerIleLeuLysArgValTyrAspIleLeuTyrIlePheLysCysIleAsnLys 378
 DB GAAAGTATATGAAAGACATCAAGGATATAGATATATCTTTAAAGAGAAATTTGTTAAA 966
 QY AlaValGlyGlyGlyValGluIleLysSerGlnArgTyrIleLeuGlyValArgLeu 398
 DB GTCTGGGACACGGCTGTCGAAATTCGATACACGATACAAACTGGAGTTCGCTG 1026
 QY TyrTyrArgValMetGluSerMetLeuLysSerGluGluArgIleSerIleGluAsn 418
 DB TATTACGAGTAATGTAATCTATGCTTAAATTAATTAATTAATTAATTAATTAATTAAT 1086
 QY PheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGlu 438
 DB TTATGCAAACTTCGAAATTCACACAACTTTTCAATATGCTTATTTGGGCTGCTGCTG 1146
 QY ValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 458
 DB GTTCTTAATGGGCAATATACCAAGCTACATCTCAAACTTCGATTCGCAACAGATTC 1206
 QY SerIleThrTrpIleCysAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIle 478
 DB TCTTTCTGATGATTTTGAATGCTTAAATTAATAAGCTTTGATTTTCAAAATGATTC 1266
 QY GluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArg 498
 DB GAAAGTTTTATCAACCAACCAAGGCACTTCACAAAGACAAATGATATAAAATTAACA 1326
 QY CysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeu 518
 DB TGTCAACATCAATCAATGCAATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
 QY IleLysGlnSerLysAspArgGlyProThrAspHisLeuSerAlaCysProLeu 538
 DB ATTAATAAATCAAAAGGACGAGAGAGAGACAACTGATCACTGATGATCTGCTGCTCT 1446
 QY AsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 558
 DB AATCTCTCTGCTGCAATAATATACACAGGACACATATGATCTTCTGCTGCTGCTGCT 1506
 QY ProLysLysGlyGlySerThrArgValAsnSerThrAlaAsnAlaGluThrGlnAla 578
 DB GCTTAAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAAATTTT 1566
 QY ThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheLys 598
 DB ACTTAAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAAATTTT 1626
 QY LysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGlu 618
 DB AATCTCTCTGCTGCAATAATATACACAGGACACATATGATCTTCTGCTGCTGCTGCT 1686
 QY HisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyr 638
 DB CACTTAATAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 1746
 QY GluLeuMetArgAspArgHisLeuAspGlnIleMetMetLysSerMetTyrGlyIleCys 658
 DB GAAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 1806
 QY LysValLysAsnIleAspLysLysPheLysIleIleValThrAlaTyrLysAspLeuPro 678
 DB AATCTCTCTGCTGCAATAATATACACAGGACACATATGATCTTCTGCTGCTGCTGCT 1866
 QY HisAlaValGluGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIle 698

QY 242 PheLeuProPheMetAspSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGln 261
DB 715 LIIAIAACCTTTTATCAAAATTCCTTCGACCTTCTAACATCTAATGACATCCACAGCTTGAA 774
QY 252 AsnLeuSerLysArgTyrGluGlnLileTyrLeuLysAsnLysAspLeuAspAlaArgLeu 281
DB 775 AATCTTCTTAAAGCATAGAAAGAAATTTATCTTAAAAATTAATATATATATATATATATAT 834
QY 282 PheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301
DB 845 TTTTGGATCATGATATAAAATCTTCAGACTGATCTATAGACAGTCTTGAAGACACAGAA 894
QY 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProPheHisThrProVal 321
DB 895 ACACACAGAAAGAAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 954
QY 342 ArgThrValMetAsnThrIleGlnGlnLeuMetIleLeuAsnSerAlaSerAspGln 341
DB 955 AGAGCTGTATGAACTATGACAAATTAATGATGATTTTAAATTCAGCAAGTATCAA 1014
QY 342 ProGlnGlnAsnGlnGlnSerIlePheAsnAspCysThrValAsnProLysGluSerIle 361
DB 1015 GCTTCAAAAATCTGATTTCTTATTTTACACACTGACAGTGTATCCAAAAGAGATATA 1074
QY 362 LeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGly 381
DB 1075 CAGAAAACAGTCAAGATATAGGATATATCTTTAAACAGAAATATCTCTAAAGCTGAGGAA 1134
QY 382 GluGlyLysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
DB 1135 CAGGTTGTGTGTAATTTGATATATAGGATATATATAGGATATATATAGGATATATAGG 1194
QY 402 ValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLys 421
DB 1195 GTATGTAATCTATGAT 1254
QY 422 LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuValValMet 441
DB 1255 GTTCTGAAAGCAACATTTTCTATATATATATATATATATATATATATATATATATATAT 1314
QY 442 AlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhePro 461
DB 1315 GGCATATATAGCAAGATATATCTCAAAATCTGATCTGGAACACATTTGCTTTCCCA 1374
QY 462 TrpIleGluAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPhe 481
DB 1375 TGGATCTGAAATGTCTTAAATTTAAATATATATATATATATATATATATATATATATAT 1434
QY 482 IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHis 501
DB 1435 ATCAAGCAGCAAGGCACTTCAGCAAGCAAAATGATATAAAATTTAGACGATGCAACAT 1494
QY 502 ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuLileLysGln 521
DB 1495 GGAATCATGAAATGCTTGGATGCTGCAATTCACATTCATTTTATGATCTATTAACAA 1554
QY 522 SerTyrAspAlaIleGluGlyThrIleAspHisLeuGluSerAlaCysProLeuAsnAlaPro 541
DB 1555 TCAAAAGCAAGCAAGCACTTCAGCAAGCAAAATGATATAAAATTTAGACGATGCAACAT 1614
QY 542 LeuGlnAsnAsnHisThrAlaAlaAspMetLysLeuSerProValArgSerProLysLys 561
DB 1615 GTCAGAAATATACACATGACCAACATATGATCTTCTCTCTGATGATCTTCTCTCTCTCT 1674
QY 562 LysGlySerThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
DB 1675 AAAGATTAAT 1734
QY 582 PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr 601
DB 1735 TTGAGACCAAGCAAGCACTTCAAAATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1794

QY 602 ArgLeuAlaTrpLeuAlaLeuAspThrLeuArgSerAlaLeuLeuSerGluHisProGln 621
DB 1795 GGGTACGCTATATCCGGCTAAATACACTTTTGCAAGCGCTTCTGCTGAGCACCAAGAA 1854
QY 622 LeuGluHisIleIleThrPhePhePheGlnHisThrIleGlnAsnGluTyrGluLeuMet 641
DB 1855 TTAAAT 1914
QY 642 ArgAspArgHisIleAspGlnIleMetMetCysSerMetCysGlyCysLysValLys 661
DB 1915 AGACACAGGATTTTGGACCAAAATATATGATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1974
QY 662 AsnIleAspLeuLysPheLysIleIleValThrAlaTrpLysAspLeuProHisAlaVal 681
DB 1975 AATATACACCTTAAATTTCAAAATCATTTGTATACACATACAAAGATCTTCTCTCAAGG 2034
QY 682 GlnClnThrPheLysArgValLeuLileLysGluGluGlyTyrAspSerIleIleValPhe 701
DB 2035 CAGGAGATATTAATTAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2094
QY 702 TyrAsnSerValPheMetGlnArgLeuLysPheAsnIleGluGluGluGluGluGluGlu 721
DB 2095 TATATCTGGCT 2154
QY 722 ProProTyrLeuSerPheIlePheHisIleThrArgSerPheTyrLysPheTyrSer 741
DB 2155 CCCCCTACCTTCT 2214
QY 742 ProLeuArgIleGluGlyCysAsnIleGlyIleSerIleLeuLysSerThrPheLysIle 761
DB 2215 CCTTATGGAATCTTCT 2274
QY 762 SerGluGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
DB 2275 TCACAAAGCT 2334
QY 782 GlyGluSerThrThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSer 801
DB 2335 CCGCAATCATCTGGGACTCTCTGACAGCTCTCTGACAAATATAATCAGATCTGATCTGAT 2394
QY 802 AspArgValLeuLysArgSerAlaGluGlySerAsnThrLysThrLysLysLysLysLys 821
DB 2395 GAGGTGTTCT 2454
QY 822 ArgPheAspIleGluGlySerArgGlnAspGlySerLysHisIlePheGluGluGlu 841
DB 2455 CCGTCTGATATGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2514
QY 842 LysPheGlnIleLysLeuAlaGluMetThrSerThrArgThrArgMetGluLysHisLys 861
DB 2515 AAATTCATGAGAAATCTCTGAGAAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2574
QY 862 MetAsnAspSerMetAspThrSerAsnLysGluGluLys 874
DB 2575 ATCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2634
RESULT 13
US-09-469 522-48
: Sequence 48, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Henedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX


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522 SerLysAspArgGlyGluProThrAspHisSerGlnSerAlaGlySerProLeuAsnLeuLeu 141
154 TAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
542 LeuGlnAsnAsnHisThrAlaAlaAspMetPyrLeuSerProValArgSerProLysLys 561
154 CACAGAGAAATACACACACAGCAGCAGATATGTAATCTTCTCTGTAAGATCTCAAGAGAA 1680
562 LysLysSerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
154 AAAGGCTCAACACAGCGGAGTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
582 PheGlnThrGlnLysSerThrSerSerThrSerSerSerSerSerSerSerSerSerSer 1800
154 TCCAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1900
582 ArgLeuAlaIleTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 621
154 CCGCTAGGCTATCTCCGCTTAAATACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
622 LeuGlnHisIleIleThrThrLeuPheGlnHisThrLeuGlnAsnAlaTyrGlnLeuMet 641
154 TTAAGAGATAATCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
642 ArgAspArgLeuLeuAspGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 661
154 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
662 AsnIleAspLeuLysPheLysIleIleValThrAlaArgLysAspLeuProHisAlaVal 681
154 AATATAGAGCTTAAATCTCAAAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2040
682 GlnGlnThrPheLysArgValLeuIleLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 701
154 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
702 TyrAspSerValPheMetGlnArgIleLysLysThrAsnIleGlnGlnGlnGlnGlnGln 721
154 TATAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
722 ProThrThrLeuSerProIleProHisIleThrCysArgSerProLysThrProGlnSer 741
154 CCGCTAGGCTATCTCCGCTTAAATACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2200
742 ProLeuArgIleProGlnGlnArgIleLysLysThrAsnIleGlnGlnGlnGlnGlnGln 761
154 CCGCTAGGCTATCTCCGCTTAAATACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2260
762 SerGlnGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
154 TCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
782 GlyLeuArgLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 801
154 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
802 ArgArgValLeuLysArgSerAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 821
154 CAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
822 ArgPheAspIleGlnGlySerAspGluAlaAspClySerLysHisLeuProGlyGluSer 841
154 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
842 LysPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 861
154 AAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
862 MetAsnAspSerMetAspThrSerAsnLysGlnGluLys 874
154 ATGAAATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2640

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RESULT 14
US-09-469-522-42
: Sequence 42, Application US/59469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESS: Arnold, White & Purkeo
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PATENTLITE RELEASE #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/469,522
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/026,459
: FILING DATE: <Unknown>
: AUTHORITY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: UTXC:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3347 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: Single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2583
: SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-469-522-42
Alignment Scores:
Pred. No.: 0 Length: 3347
Score: 4103.50 Matches: 803
Identical Similarity: 91.98 Conserving: 0
Best Local Similarity: 91.98 Mismatches: 1
Query Match: 91.1% Indels: 69
DB: 10 Gaps: 1
US-09-026-459a-31 (1-874) x US-09-469-522-42 (1-3347)
QY 2 AsphethrAlaIleuCysGlnLysLeuLysIleProAspHisValArgGlnArgAlaIle 21
Db 172 GATTTTACTGATTATGTCAGAAATTAAGATACAGATCATGTCAGAGAGAGAGAGATGG 231
QY 22 LeuThrTrpGlnLysValSerSerValAspGlyValLeuGlyGlyTyrIleGlnLysLys 41
Db 232 TTAAGTCCACAGAACTTCACTGTCGCAAGCAGATAGGAGCGTTATATCAAAAGAAA 291
QY 42 LysGlnLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspGlnMetSerPhe 61
Db 392 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 242
QY 62 ThrIleThrGlnLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeu 81

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1027 553GGGCGTCTGCAAGGAGCAATATAGCAGACGATACATCGAATCTTCAT 1086
1028 553GGGCGTCTGCAAGGAGCAATATAGCAGACGATACATCGAATCTTCAT 1086
454 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 473
1087 454SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 473
1088 454SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 473
474 PheTyrLysValIleGlnSerPheIleLysAlaGlnLysAsnLeuPheArgGlnMetIle 493
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Job time : 152.801 secs

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RESULT 4
US-09-860-211-7
Sequence 7, Application US/09860211
Patent No. US-600-49137212A1
GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
Maneval, Daniel C.
Willis, Ken N.
TITLE OF INVENTION: Recombinant Adenoviral Vector and
METHOD OF USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,211
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,673
FILING DATE: 15-FEB-2000
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-OCT-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,367
KIP/LAUNCH/DOCK/LI NUMBER: 016930 00092005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 574-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

[illegible]

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RESULT : 6
US : 09 469 522 28
: September 28, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
:
: TITLE OF INVENTION: MODIFIED PEPINOBLASTOMA TUMOR SUPPRESSOR
: PROTEINS

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RESULT 9
US 09 469 522 40
: Sequence 40, Application US/09469522
: Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210 4434
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hubler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/WORK NUMBER: UTXC-506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-5000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2528
SEQUENCE DESCRIPTION- SEQ ID NO: 40-
US 09 469 522 40

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Alignment Scores:
Prod. No.: 0 Length: 3392
Score: 4156.50 Matches: 812
Percent Similarity: 93.14% Conservatave: 1
Best Local Similarity: 93.01% Mismatches: 1
Query Match: 92.33% Indels: 59
ID: 10 Gaps: 1

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1490 TGGATTCGAAATGCTTAAATTTAAAGCCTTTGATTTTACAAAGTATGATCCTTTTCC 1449
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2470 GGTTTGATATTGAGAGATTTTASAGATTTTASAGATTTTASAGATTTTASAGATTT 2529
837 LysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLys 856
2530 AATTTTCAGTAAATTTGAGAGATTTTASAGATTTTASAGATTTTASAGATTTTASAG 2589
857 MetAsnAspSerMetAspThrSerAsnLysGluGluLys 869
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RESULT 10
US-09-469,520-42
Sequence 42, Application US/09/469522
Patent No. US20030151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED KETINOLASINOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41-071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs


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674  HisAlaValGlnGlnThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIle 693
1867  CATGGCTGTCAGAGAAATTCGAAGCTTTTTCATTAAGAGAGAGAGATGATGATTTTATT 1926
694  IleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAla 713
1927  ATAGTATTCATTAAGCTGCGCTTCATGACAGACTCAAAACAAATATTTTCACATAGCT 1986
714  SerThrArgProThrLeuSerProIleProHisIleProArgSerProTyrLysPhe 733
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 Job time: 156.436 secs

Sequence version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein: nucleic search, using frame_plus.pzn model

Run on: January 18, 2003, 04:31:54 : Search type: 4, 523 seconds
(without alignments)
6107.852 Million cell updates/sec

Library: US 09 026 459A 49

Perfect score: 4496

Sequence: 1 MPRKPRKIAIAAAAAEP.....IMOKRMNDISINKEEK 871

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Wgapop: 10.0 : Wgapext: 0.5

Edgapop: 6.0 : Edgapext: 7.0

Delgap: 6.0 : Delext: 7.0

Searched: 93868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 9%

Maximum Match 100%

Listed first 4% summaries

Command line parameters:

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DB-published Applications NA -GEMT-fastap -SUFFIX-rnpb -MINMATCH-0.1

TRANS human40,cds -L15P-45 -LOCAL-200 -THR SCORP-pet -THR MAX-100

THR MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pet -NORM-ext -HEAPSIZE-500 -MINLEN-0

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DEV TIMEOUT 120 WARN TIMEOUT-40 -THREADS 1 XGAPOP-10 XGAPEXT-0.5 -FCGAPOP-6

FCGAPEXT 7 XGAPOP-10 XGAPEXT-0.5 DELGAP-6 -DELEXT-7

List those:

Published Applications_NA:

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2	4447.5	98.9	4555	10	US 09 469 522-1	Sequence 1, Appl
3	4447.5	98.9	4889	9	US 09 954 541-14	Sequence 143, App
4	4447.5	98.7	2995	10	US 09 860 241-7	Sequence 7, Appl

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	4447.5	98.9	4555	10	US 09 469 522-1	Sequence 1, Appl
3	4447.5	98.9	4889	9	US 09 954 541-14	Sequence 143, App
4	4447.5	98.7	2995	10	US 09 860 241-7	Sequence 7, Appl

5	4447.5	98.7	3554	10	US 09 469 522 50	Sequence 50, Appl
6	4259.5	94.7	3455	10	US 09 469 522 28	Sequence 28, Appl
7	4256	94.7	3461	10	US 09 469 522 40	Sequence 40, Appl
8	4166	92.7	3477	10	US 09 469 522 46	Sequence 46, Appl
9	4149.5	92.3	3392	10	US 09 469 522 40	Sequence 40, Appl
10	4052	90.3	3347	10	US 09 469 522 42	Sequence 42, Appl
11	4017.5	89.4	3323	10	US 09 469 522 38	Sequence 38, Appl
12	4004	88.6	3323	10	US 09 469 522 38	Sequence 38, Appl
13	3923.5	87.3	3266	10	US 09 469 522 34	Sequence 34, Appl
14	3832.5	85.5	3238	10	US 09 469 522 3	Sequence 3, Appl
15	3799	84.5	3161	10	US 09 469 522 44	Sequence 44, Appl
16	3667.5	81.6	3113	10	US 09 469 522 36	Sequence 36, Appl
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19	515.5	11.5	3747	12	US 10 025 676 2	Sequence 2, Appl
20	375	8.3	3294	10	US 09 250 091 4	Sequence 4, Appl
21	243	5.4	411	10	US 09 864 761 4141	Sequence 4141, Ap
22	218	4.8	129	10	US 09 864 761 19910	Sequence 19910, A
23	177.5	3.9	304	10	US 09 963 824A 296	Sequence 296, App
24	145.5	3.2	324	9	US 09 794 692 2546	Sequence 2546, Ap
25	145	3.2	9274	10	US 09 885 535 3	Sequence 3, Appl
26	142.5	3.2	2637	10	US 09 815 245 9859	Sequence 9859, Ap
27	142.5	3.2	10096	10	US 09 960 253 164	Sequence 164, App
28	142.5	3.2	10390	10	US 09 864 863 292	Sequence 292, App
29	142.5	3.2	10211	10	US 09 954 456 1154	Sequence 1154, App
30	142.5	3.2	10211	10	US 09 967 768A 186	Sequence 186, App
31	141	3.1	4754	10	US 09 982 091A 1	Sequence 1, Appl
32	140.5	3.1	8493	9	US 10 071 766 51	Sequence 51, Appl
33	136	3.0	3624	9	US 10 108 605 216	Sequence 216, App
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36	133.5	3.0	3996	10	US 09 801 368 369	Sequence 369, App
37	131.5	2.9	2047	10	US 09 864 761 32004	Sequence 32004, A
38	131	2.9	1969	10	US 09 864 761 15490	Sequence 15490, A
39	130	2.9	7747	10	US 09 960 253 43	Sequence 43, Appl
40	130	2.9	7747	10	US 09 960 253 175	Sequence 175, App
41	130	2.9	7742	12	US 10 044 090 359	Sequence 359, App
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45	125.5	2.8	2595	9	US 10 033 297 20	Sequence 70, Appl

ALIGNMENTS

RESULT 1

US-09-469 522-48
Sequence 48, Application: US/094/9522
Patent No. US5920151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED REIN-BLASTOMA TUMOR SUPPRESSOR
PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENT ADDRESS:

ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: IBM DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22 Dec 1999

CLASSIFICATION: <Unknown>

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 564 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 583
 1867 CGTGAATATCT 1926
 584 ProLeuLysSerThrSerLeuSerLeuPheTyrosLysValTyrArgGluAlaTyrLeu 603
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 1987 CGCTAAATATCT 2046
 624 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 643
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 664 PheLysIleLeuValThrAlaTyrLysAspLeuPheHisAlaValGlnGluThrPheLys 683
 2167 TTCAAATCT 2226
 684 ArgValLeuIleLysLeuGluThrAspSerIleLeuValPheTyrAsnSerValPhe 703
 2227 CGTCT 2286
 704 MetGlnArgLeuLysThrAsnIleLeuGlnIleValAlaSerThrArgProProThrLeuSer 723
 2287 ATCTACATCT 2346
 724 ProLeuProHisIleProArgSerProGlyLysPheProSerProLeuArgIlePro 743
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 2407 GGACGCAATCT 2466
 764 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly 783
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QY 864 ArgSerAlaGluGlySerAspProProGlySerProLeuLysLysLeuArgPheAspIleGlu 823
DB 2587 ACAAGGTCGAAGCAAGCAACCCCTCAACCACTCAAAAACTAGCCTTCATATTCGA 2646
QY 824 GlySerAspGluAlaAspGlySerLysLysLeuProGlyGlySerLysPheGlnGlnLys 843
DB 2647 GATATCATAAAGCATATGATCAATCAATATCTCCAGGACAGTCAAAATTTTAAAGAA 2706
QY 864 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 863
DB 2707 GAGCAAAAGATTTTATCTCAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAAT 2766
QY 864 AspThrSerAsnLysGlnGlnLys 871
DB 2767 GATACCTCAACCAAGCAAGCAAA 2790

RESULT 6
US 09-026-459-522-28
Sequence 28, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Inventor: Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
ORIGIN:
ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-0469522
FILING DATE: 22-Dec-1999
CLASSIFICATION: 20460000
APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Hubler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UIC:506
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
E-MAIL: N.P.R. SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 3455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2691
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US 09-026-459-522-28

Alignment Scores:
Aligned No.: 0 Length: 3455
Score: 4259.50 Matches: 837
Percent Similarity: 93.62% Conservative: 0
Best Local Similarity: 93.62% Mismatches: 0
Query Match: 94.74% Indels: 57

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US-09-026-459A-49 (1-871) x US 09 459 522 28 (1-3455)
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DB 70 CCTCAITTTTACTGCAITTTATGTCAGAAATTAACATACCAGATCATGTCAGAGAGAGAGAG 129
QY 75 TrpLeuThrTrpGlnLysValSerSerValAspGlyValLeuGlyGlyGlyTrpIleGlnLys 94
DB 130 TGGTTAACTGGCCAGAAAGCTTCATGCTGCGATGAGACTATTGGGACCTTATATTCAGAAAG 189
QY 95 LysLysGluLeuGlyTrpGlyIleCysIlePheIleAlaValAspPheAspGluMetSer 114
DB 190 AAAAAGCAATTTGGGCAATCTGTATTTTATTTAGTAAATAGTAAATAGTAAATAGTAAAT 249
QY 115 PheThrPheThrGluLeuGlnLysAsnIleGlnIleSerValHisLysPhePheAsnLeu 134
DB 250 TTCACITTTTACTGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309
QY 135 LeuLysGluLeuAspThrSerThrLysValAspAsnAlaMetSerArgLysLeuLysLys 154
DB 310 CTAAGCAAAATTCATACATACCAAAAGTGTATTAAGTATGTCAGAGAGAGAGAGAGAGAG 469
QY 155 TyrAspValLeuPheAlaLeuPheSerTrpGlyGluArgThrCysGluLeuIleGlyLeu 174
DB 370 TATGATGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 429
QY 175 ThrGlnProSerSerSerSerThrGluIleAsnSerAlaLeuValLeuLysValSer 194
DB 430 ACACACCCAGCAGCAGTTCGATATCTACAGAAATAATTCGTCATTCGTCGTCGTCGTCGTCG 489
QY 195 TrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGlnAspPheValLeu 214
DB 490 TGGATCACAATTTTTTATTAGCTAAAGGCGAAGTATTACAAATGGAGAGATCATCTGCTGAT 549
QY 215 SerPheGlnLeuMetLeuGlyValLeuAspTrpPheIleLysLeuSerThrMetSer 234
DB 550 TATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 609
QY 235 LeuLysGluThrProTrpLysTrpSerSerSerSerSerSerSerSerSerSerSerSer 243
DB 610 CTCAGAGCAACCATATAAAGAGCTGTATTAAGCAATAAAGTTCAGCTGAGAGAGAGAGAGAG 669
QY 243 ----- 243
DB 670 CGAGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
QY 243 ----- 243
DB 730 GAATTTCTGTAAAGATATCATATATATATATATATATATATATATATATATATATATAT 789
QY 244 ----- AsnSerLeuGlyGluValLeuSerAspGlyPheProGluVal 257
DB 790 AATTTTATACCTTTTATGAATTCCTTCGACCTTGTAACATCTAATGAGACTTCAGAGCT 849
QY 258 GluAsnLeuSerLysArgTrpGluGluIleTrpLeuLysAsnLysAspLeuAspArg 277
DB 850 GAAAATCTTTCTAAAGCATACGAGAGAAATTAATCTTAAAGATAAAGATACAGATACAGAG 309
QY 278 LeuPheLeuAspHisAspLysThrLeuGlnThrAspSerLeuAspSerPheGlnGln 297
DB 910 TTATTTTTCATATATATAAAATCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 369
QY 298 ArgThrProArgLysSerAsnLeuAspGluGluValLeuIleProHisThrPro 317
DB 970 AGAAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
QY 318 ValArgThrValMetAsnThrIleGlnGlnLeuMetMetLeuAsnSerAlaSerAsp 337

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584  protLeuYssThrSerLeuSerLeuPheTyrLeuYssValTyrArgLeuAlaTyrLeu 603
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1780  CCGCTAAATACAGTTTGCAACCCCTCTCTGAGCAGCCAGAAATACAAATATATCATC 1839
624  TrpThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMetArgAspArgHisLeu 643
1840  TGGACCGTTTTCAGACACAGCCCTGCAAGATGAGTATGCACTCATCAGACACAGCCATTTC 1899
644  AspLeuIleMetMetCysSerMetMetMetTyrLeuCysYssValTyrAsnThrAspLeu 663
1900  GAGCAAAATTAATGATGTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1959
664  PheLeuIleLeuValThrAlaTyrTyrAspLeuPheHisAlaValGluGluThrPheLeu 683
1960  TTTTAAATCAATGTAATAGCATACAGATACAGATGATGATGATGATGATGATGATGATGAT 2019
684  ArgValLeuIleLeuGluGluGluThrAspSerIleIleValPheTyrAsnSerValPhe 703
2020  CGTGTTTGAACAAACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2079
704  MetThrArgProGluThrAsnThrThrThrThrThrThrThrThrThrThrThrThrThr 723
2080  ATGACAGATGAAATATATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 2139
724  ProLeuIleHisIleProArgSerProTyrLeuPheProGluSerSerProLeuArgIlePro 743
2140  TCAATATCTACATCTGCAACCCCTTACAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2199
744  GlyThrAsnThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 763
2200  GGAAGCAATATATATATGACCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2259
764  ThrProThrIleYssMetThrProArgSerArgIleLeuValSerIleCylSerPheGly 783
2260  ACATCAATATAATATATATATATATATATATATATATATATATATATATATATATATAT 2319
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804  ArgSerAlaThrIleThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 823
2380  AGAAGTCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2439
824  CysSerAspThrAlaAspCylSerThrHisIleProGluThrSerThrSerThrSerThrSer 843
2440  GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2499
844  LeuAlaGluMetThrSerThrArgThrArgMetGlnIleYssIleYssMetAsnAspSerMet 863
2500  CTGGCAACAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2559
864  AspThrSerAsnIleGluLeuYss 871
2560  CATACCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2583

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RESULT 11

US-09-026-459-522 42

Sequence 32, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Inventor: Xu, Hong-Ji

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APP. NO. IN NUMERICAL ORDER: 35,000,000, 522
FILING DATE: 22-Dec-1999
CLASSIFICATION: C12N 2501/00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
FAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME: FLY_CDS
LOCATION: 7..2559
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-469-522-32

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Alignment Scores:
Pred No. 0 Length: 3323
Score: 4017.50 Matches: 793
Percent Similarity: 93.22% Gaps: 0
Best Local Similarity: 93.22% Mismatches: 0
Query Match: 93.35% Indels: 57
DB: 10 Gaps: 2

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US-09-026-459a-49 (1-971) x US-09-469-522-32 (1-3323)

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Db 70 TGGGAAATCTGATCTTTATTCAGCAGTTGACCTACATGACATGCTGCTGCTGCTGCT 129
QY 119 GluLeuGluLysAsnIleGluIleSerValHisLysPhePheAsnLeuIleLeu 138
Db 130 GAGTACAGAAACATAGAAATAGTGTCTTAAATTTTAACTTAACTTAACTTAACTTAA 189
QY 139 AspThrSerThrIleValAspAsnAlaMetSerArgCysCylCylYssIleValLeu 158
Db 140 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 249
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Db 250 TTTCACCTCTTTCAGCAATTTGGAAACGACATGTAACATTAATTAATTAATTAATTA 309
QY 179 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPhe 198
Db 310 AGTTCATATATATGAAATATATGATTTGCTTGGTAAAGTTTCTTGGTACACATTT 469
QY 199 LeuLeuAlaLysCylGluValLeuGluMetGluAspAspLeuValIleSerPheGluLeu 218

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RESULT 13

US-09-469-522-44

Sequence 34, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

In, Shi-Xue

Benedict, William F.

Zhong, Yunli

TITLE OF INVENTION: MODIFIED RETINOL-INDUCED TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Dorkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: -Unknown-

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: -Unknown-

ATTORNEY/AGENT INFORMATION:

NAME: Hiblot, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: 01X0506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 3266 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

[illegible]

Search completed: January 19, 2003, 05:47:54
Job time : 156.582 secs

Sequence 4, Application US/0601092
 Patent No. 6074950
 GENERAL INFORMATION:
 APPLICANT: Autolman, Douglas
 APPLICANT: Gregory, Richard J.
 APPLICANT: Mills, Kenneth N.
 TITLE OF INVENTION: Tissue Specific Expression of
 TITLE OF INVENTION: Retinoblastoma Protein
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/0601092
 FILING DATE: 14 FEB 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/750 537
 FILING DATE: 15 NOV 1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Ellis, Reese A.
 REGISTRATION NUMBER: 35,146
 REFERENCE/DOCKET NUMBER: 016940-001020
 TELEPHONE/DOCKET INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 704-576-0400
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2994 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US 08 061 092 4

Alignment Scores:
 Seq. No.: 0 Length: 2994
 Score: 4609.00 Matches: 894
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.89% Indels: 0
 Gaps: 4

US 09 026 459A 29 (1 895) x US 08 801 092 4 (1-2994)
 29 2 GluAspSerGlyProGluAspLeuProGluValArgLeuGluPheGluGluThrGluGlu 21
 10 241 CAGACACACAGACAGAC 400
 29 22 ProAspPheThrAlaLeuGlyGlnLysLysLysLysLysLysLysLysLysLysLysLys 41
 10 301 CCGTATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 460
 29 42 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 61
 10 461 TGGTAACTTTGGACACAAATTTTCACTGTGGAGAGAGATTTGGAGAGATTTTCAAAAG 420
 29 62 LysLysGluLeuTrpGlyIleGlySerPheIleAlaValAspLeuAspGluMetSer 81
 10 421 AAAAAGCAACGCGCGGCAACCGTATGATGATGATGATGATGATGATGATGATGATGATG 480
 29 82 PheThrPheThrGluLeuGlnLysAsnIleGluSerValHisLysPhePheAsnLeu 101
 10 1561 AAATCTGCGATGACAAATTTTCTTATATGCTTTATATGCTTTATATGCTTTATATGCTTTAT 162

Db 481 TTCATTTTATGTAGCTATAGAAAAATATAGAAAAATATAGAAAAATATAGAAAAATATAG 540
 QY 102 LeuLysGluLeuAspSerThrLysValAspSerAlaMetSerAlaLeuGluGlySer 121
 Db 541 CAAAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 122 TyrAspValLeuPheValLeuPheSerLysLeuGluAlaThrGlyGlnGluIleTyrLeu 141
 Db 601 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 142 ThrGlnProSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 161
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 Db 721 TCGATCACAATTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 182 SerPheGlnLeuMetLeuMetLeuMetLeuMetLeuMetLeuMetLeuMetLeuMetLeu 201
 Db 781 TCATTTTCATTAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 840
 QY 202 LeuLysGluLeuPheThrAlaValIleThrGlnGluAsnIleGluAlaTrpAla 221
 Db 841 CCAAGAAACAT 900
 QY 222 ArgGlyCysLeuAspSerAlaValIleAlaGlyGlnGluAlaThrAspSerAlaVal 241
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 Db 961 GAATTTCTTTTAAAGAAATCAAGCTTAAATATAGATCACTCAAAAAATCTTATTTTAAA 1020
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10 961 GAAATGCTGCAAAACAAACAGAAAGTAAATGATGAGGCAAGGAAAGGATTAATTCAAA 1020
27 262 AAGPheIleProPheMetAsuSerLeuGlyValThrSerAsuGlyLeuProGlyVal 281
10 1021 AATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1080
27 282 GlnAsnLeuSerTyrAspGlyThrLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 301
10 1081 GAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1140
27 302 GlnPheLeuAspHisAspGlyThrLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 321
10 1141 TTAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1200
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10 1201 AAGAACACCAAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1260
27 342 ValArgThrValMetAsuThrIleGlnGlnLeuMetMetIleLeuAsuSerAlaSerAsp 361
10 1261 GTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
27 362 GlnProSerGlnAsuLeuIleSerTyrPheAsuAsuGlyThrValAsuProLysGluSer 381
10 1321 CAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1380
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10 1381 AATGCAAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1440
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10 1441 GAAACGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
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10 1501 CAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1560
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10 1621 ATGACCAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1680
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10 1681 CAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1740
27 502 PheIleLysAlaGlnGlyAsuLeuThrArgGlnMetIleLysHisLeuGlnArgCysGln 521
10 1741 TTAATGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1800
27 522 HisArgIleMetGluSerLeuAlaThrPheLeuSerAspSerProPheAspLeuIleLys 541
10 1801 CAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 1860
27 542 GlnSerLysAspArgGlnGlyProThrAspHisLeuGlnArgAlaLysThrLeuAsuLeu 561
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27 582 LysLysLysSerThrThrArgValAsuSerThrAlaAsuAlaGlnThrGlnAlaThrSer 601
10 1981 AAAAAAGGTTAACTGAGGTTAACTGAGGTTAACTGAGGTTAACTGAGGTTAACTGAGGTTAA 2040
27 602 AlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysVal 621

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10 2041 GCTTCCACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 2100
27 622 TyrArgLeuAlaTyrLeuArgLeuAsuThrLeuGlyValAlaLeuLeuLeuSerGlnHisPro 641
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10 2401 TCTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2460
27 742 ArgProThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSer 761
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10 2761 CTACGCTTATGATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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10 2821 TCATAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
27 882 LysMetAsuAspSerMetAspThrSerAsuLysLeuLysLys 895
10 2881 AAAAAAGGTTAACTGAGGTTAACTGAGGTTAACTGAGGTTAACTGAGGTTAACTGAGGTTAA 2942

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RESULT 6

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1. Sequence 1, Application 16/HUS9410467
2. GENERAL INFORMATION:
3. APPLICANT: The Regents of the University of California
4. APPLICANT: and Cadi, Inc.
5. TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
6. NUMBER OF SEQUENCES: 3
7. CORRESPONDENCE ADDRESS:
8. ADDRESSEE: Campbell and Flores
9. STREET: 4370 La Jolla Village Drive
10. CITY: San Diego
11. STATE: California
12. COUNTRY: USA

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1 ZIP: 92129
 2 COMPUTER READABLE FORM:
 3 MEDIUM TYPE: Floppy disk
 4 COMMENTS: IBM PC compatible
 5 OPERATING SYSTEM: PC-DOS/MS-DOS
 6 SOFTWARE: PatentIn Release #1.0, Version #1.25
 7 CURRENT APPLICATION DATA:
 8 APPLICATION NUMBER: PCT/US94/10357
 9 FILING DATE: 13-SEP-1994
 10 CLASSIFICATION:
 11 PRIOR APPLICATION DATA:
 12 APPLICATION NUMBER: US 08/121,108
 13 FILING DATE: 13-SEP-1994
 14 ATTORNEY/AGENT INFORMATION:
 15 NAME: Campbell, Cathryn A.
 16 REGISTRATION NUMBER: 31,815
 17 REFERENCE TO OTHER PCT NUMBERS: PCT/US 94/117
 18 TELECOMMUNICATION INFORMATION:
 19 TELEPHONE: (619) 535-9001
 20 TELEFAX: (619) 535-8949
 21 INFORMATION FOR SEQ ID NO: 1:
 22 SEQUENCE CHARACTERISTICS:
 23 LENGTH: 2994 base pairs
 24 TYPE: nucleic acid
 25 STRANDEDNESS: single
 26 TOPOLOGY: linear
 27 FEATURE:
 28 NAME/KEY: CDS
 29 LOCATION: 139..2923
 30 PRT-US94-10357-1

Alignment Scores:

1 Pct. No.: 0 Length: 2994
 2 Score: 4606.00 Matches: 893
 3 Percent Similarity: 100.00% Conservative: 1
 4 Best Local Similarity: 99.89% Mismatches: 0
 5 Query Match: 99.83% Indels: 0
 6 Gaps: 5

US 09-026-459A-29 (1-895) x PCT-US94-10357-1 (1-2994)

23 2 AlaAspSerGlyProHisAspLeuProLeuValAlaLeuGluPheGluGluThrGluGlu 21
 24 241 CAGAAACAGAGCGGAGAGAGCTGTCTTGTGAGCTTAACTTAAAGAAACAGAGAA 300
 25 22 ProAspPheThrAlaLeuGlyCysGlnIleCysIleProAspHisValArgGluArgAla 41
 26 601 CTGATTTTATGTGATTATGTCAGAAATTAAGATACCAATCATGTCAGAGAGAGAGGT 360
 27 42 TrpLeuThrTrpGluLysValSerSerValAcpGlyValLeuGlyGlyTyrIleGlnLys 61
 28 601 TGGTAAATTCGGCAATAAGCTTTCATGTCGATGGAGTATTCGACGTTATATTCAAAAG 420
 29 62 LysLysGlnLeuArgGlyIleCysIleLeuAlaValAlaPheAlaPheAlaSer 81
 30 441 AAAAGAGAAATGTGGGAATCTGATCTTTATTCGAGAGCTTGAATGATGATGATGATG 480
 31 42 PheThrThrGluGlnGlnIleCysIleGluIleSerValHisLysPhePheAsnLeu 101
 32 441 TTCACTTTTATGTAGCTACACAAAACATAGAAATCAGTGTCCATAAATCTTTAACTTA 540
 33 102 LeuLysGlnIleAspThrSerThrLysValAlaAspAsnAlaMetSerArgLeuLysLys 121
 34 441 CAAAAAATTCATACAGATACCAAACTTCATTAAGCTAAGCTAAGCTAAGCTAAGCTA 600
 35 122 TyrAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGlnLeuIleTyrLeu 141
 36 441 TATGATGATATTTTGTGCTTCTTCTGCAAAATTCAGAAATTCAGAAATTCAGAAATTC 660
 37 142 ThrIleProSerSerSerIleSerThrGluIleAsnSerAlaLeuValIleLysValSer 161
 38 441 ACAAAACACATTCGATATGTTATGAAATTAATTCATTCATTCATTCATTCATTCATTC 720

23 162 TrpIleThrPheLeuLeuAlaLysGlyGluValIleuGluAspLeuValIleP 181
 24 721 TGGATCACATTTTATTAAGCTAAAGGGAAGTATTAACAAATGGAAGATGATGATGAT 780
 25 182 SerPheGlnLeuMetCysCysValLeuAspTyrPheIleLysLeuSerProMetLeu 201
 26 781 TCATTCAGTTAAATGCTAIGTGGCTTGAATTAATTAATTAATTAATTAATTAATTAAT 840
 27 202 LeuLysGlnIleProTyrTyrThrAlaValIlePheIleAspGlySerThrGlyPhe 221
 28 841 CTCAAAGAACATATAAAGACGCTTATACCCATTAATGCTTCACTGCAATACCAAG 900
 29 222 ArgGlyGlnAsnArgSerAlaValLeuLysGlnLeuGluAspThrAlaValIle 241
 30 961 CTAGGCTCAGAACAGGAGAGCTAGCAAGAACTACAAAATGATACACAAATTAAT 960
 31 342 GluValLeuGlyLysGlnHisCysCysAspIleAspGluValLysAsnValTyrPhe 261
 32 961 GAAGTTCTCTGTAAGAAACATGAATGATATATATATATATATATATATATATATAT 1020
 33 262 AsnPheIleThrPheMetAspSerLeuGlyLeuValIleSerAspGlyLeuGlnVal 281
 34 1021 AATTTTATACCTTTTATGAATTTCTTGGACCTTGTAACTATTAATGATGATGATGAT 1080
 35 382 GlnAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAspLysAspLeuAspAla 301
 36 1081 CAAAATCTTCTTAAACGATACGAAGAAATTTATCTTAAATTAATTAATTAATTAAT 1140
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RESULT 10

US-09-026-459a-29.rni

Sequence 1: Application US/08470091

Patent No. 5912236

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

INVENTOR: Hu, Shi-Xue

ADDRESS: Hengshui, Beijing, P.R.

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

METHODS FOR Tumor Suppressor Gene Therapy.

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

METHODS FOR Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

INFORMATION FOR SEQ ID NO:

APPLICATION NUMBER: US/08470091

FILING DATE: JUN-16-1995

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

PRIORITY NUMBER: 08/038,760

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Messner, Brian M

REGISTRATION NUMBER: 28,462

REFERENCE/SEQUENCE NUMBER: 7409 025 999

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4242 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

REMARKS: not relevant

MOLECULE TYPE: DNA

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FEATURE:
NAME/KEY: CDS
LOCATION: 19...2469
US-08-470-091-1
Alignment Scores:
Pred. No.: 0
Score: 4213.00
Length: 3232
Percent Similarity: 100.00%
Matches: 820
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 91.31%
Indels: 0
Gaps: 0
US-09-026-459a-29 (1-995) v US-08-470-091-1 (1-3232)

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